



DR WPI; 2003-689603/65.  
 DR N-PSDB; AAD58607.  
 XX  
 PT New isolated molecule comprising an antibody that binds with a human  
 PT major histocompatibility complex (MHC) class I being complexed with a HLA  
 PT -restricted antigen, useful for treating cancer, viral infection or  
 PT autoimmune disease.  
 XX  
 PS Claim 63; Fig 3a; 81pp; English.  
 XX  
 CC The invention relates to an isolated molecule comprising an antibody  
 CC specifically bindable with a binding affinity below 20 nanomolar to a  
 CC human major histocompatibility complex (MHC) class I being complexed with  
 CC a HLA-restricted antigen. The molecules, antibodies, and methods are  
 CC useful for treating cancer, viral infection and an autoimmune disease.  
 CC The invention is useful in gene therapy. The present sequence is mouse G1  
 CC single chain Fv-recombinant antibody  
 XX  
 SQ Sequence 237 AA;  
 Query Match 100.0%; Score 1272; DB 7; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-83;  
 Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QVTLQESGGGLVPRGSLKLSCAASGFTFSSYGMWVRQTPDKRLKLEWVATISSGGSYTY 60  
 DB 1 QVTLQESGGGLVPRGSLKLSCAASGFTFSSYGMWVRQTPDKRLKLEWVATISSGGSYTY 60  
 QY 61 PDSVKGKFTISRDNKNTLYLQMSLKSEDTAMTYCARGNWEGWYFDVWGQGTIVTVSSG 120  
 DB 61 PDSVKGKFTISRDNKNTLYLQMSLKSEDTAMTYCARGNWEGWYFDVWGQGTIVTVSSG 120  
 QY 121 GGGSGGGGGGGGSGNIELTQSPAIMSASPGERVMTCSASSIRYIYWQOKRGSPPRL 180  
 DB 121 GGGSGGGGGGGGSGNIELTQSPAIMSASPGERVMTCSASSIRYIYWQOKRGSPPRL 180  
 QY 181 IYDTSNVAAGVPRFSGSGSGTSYSTLTINRMEADATYYCQEWGYPYTFGGGTGL 237  
 DB 181 IYDTSNVAAGVPRFSGSGSGTSYSTLTINRMEADATYYCQEWGYPYTFGGGTGL 237  
 RESULT 2  
 AAE33333  
 ID AAE33333 standard; protein; 281 AA.  
 XX  
 AC AAE33333;  
 XX  
 DT 02-APR-2003 (first entry)  
 XX  
 DE 12B antibody.  
 XX  
 KM MUC-1; 12B; variable light domain; VL; variable heavy domain; VH;  
 KM diabody; cancer; antibody; therapy.  
 XX  
 OS Unidentified.  
 XX  
 OS Unidentified.  
 XX  
 PN MO200279429-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 28-MAR-2002; 2002W0-US009735.  
 XX  
 PR 30-MAR-2001; 2001US-0280721P.  
 XX  
 PA (REGC ) UNIV CALIFORNTA.  
 XX  
 PI Denardo SJ, Winthrop MD, Denardo GU;  
 DR WPI; 2003-046804/04.  
 DR N-PSDB; AAD50925.  
 XX  
 PT Novel antibody that specifically binds to cancer antigen MUC-1 useful for  
 PT detecting a cell bearing MUC-1 antigen, comprises variable light or

PT variable heavy domains of antibodies 12E, 3D, A5 or C4.  
 XX  
 XX Claim 67; Page 16; 75pp; English.  
 XX  
 CC The invention relates to a novel antibody that specifically binds to the  
 CC cancer antigen MUC-1. The antibody comprises a domain having a sequence  
 CC of a polypeptide selected from 12E variable light (VL) or variable heavy  
 CC (VH) domain, 3D VL or VH domain, A5 VL or VH domain and C4 VL or VH  
 CC domain. Antibodies of the invention are useful for detecting a cell  
 CC bearing a MUC-1 antigen. The invention is useful for producing a variety  
 CC of human or humanised antibodies or diabodies. The invention is also  
 CC useful for treating cancer. The present sequence is 12E antibody  
 XX  
 SQ Sequence 281 AA;  
 Query Match 77.4%; Score 984; DB 6; Length 281;  
 Best Local Similarity 77.2%; Pred. NO. 1.2e-62;  
 Matches 183; Conservative 24; Mismatches 30; Indels 0; Gaps 0;  
 QY 1 QVTLQESGGGLVPRGSLKLSCAASGFTFSSYGMWVRQTPDKRLKLEWVATISSGGSYTY 60  
 DB 23 QVTLQESGTEVVRGASVTLSCASGIRFTSYDIDVVRQTPDGLGEMIGWIFPGEGSTEV 82  
 QY 61 PDSVKGKFTISRDNKNTLYLQMSLKSEDTAMTYCARGNWEGWYFDVWGQGTIVTVSSG 120  
 DB 83 NEKFKGRATLSYDKSSSTAYMELRLTSBDSAYVFCARGDYRRYRFDLWGQGTIVTVSSR 142  
 QY 121 GGGSGGGGGGGGSGNIELTQSPAIMSASPGERVMTCSASSIRYIYWQOKRGSPPRL 180  
 DB 143 GGGSGGGGGGGGSDIELTQSPAIMSASPGERVMTCSASSIRYIYWQOKRGSPPRL 202  
 QY 181 IYDTSNVAAGVPRFSGSGSGTSYSTLTINRMEADATYYCQEWGYPYTFGGGTGL 237  
 DB 203 IYDTSNVAAGVPRFSGSGSGTSYSTLTINRMEADATYYCQEWGYPYTFGGGTGL 259  
 RESULT 3  
 AAB11398  
 ID AAB11398 standard; protein; 255 AA.  
 XX  
 AC AAB11398;  
 XX  
 DT 22-FEB-2001 (first entry)  
 XX  
 DE E. coli expression plasmid pUBS520-ScFvOx encoded protein.  
 XX  
 KM Eukaryotic protein; protease; interferon; antibody; hormone;  
 KM disulfide bridge.  
 XX  
 OS Escherichia coli.  
 OS Synthetic.  
 XX  
 PN EP1048732-A1.  
 XX  
 PD 02-NOV-2000.  
 XX  
 PF 26-APR-1999; 99EP-00107412.  
 XX  
 PR 26-APR-1999; 99EP-00107412.  
 XX  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 XX  
 PI WPI; 2000-674185/66.  
 DR N-PSDB; AAC66074.  
 XX  
 PT Preparation of water-soluble eukaryotic polypeptides with disulfide  
 PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the  
 PT presence of arginine or amide compound.  
 XX  
 PS Example 6; Page 22-23; 40pp; German.  
 XX  
 CC This invention describes a novel preparation of a water-soluble,  
 CC naturally occurring eukaryotic polypeptide containing two or more

CC cysteine-rich bound via a disulfide bridge which comprises cultivation  
CC of prokaryotic cells in the presence of arginine or an amide compound.  
CC The method is useful for the preparation of eukaryotic proteins e.g.  
CC proteases, interferons, protein hormones, antibodies or antibody  
CC fragments (e.g. a single chain Fv fragment that binds to thyroid  
CC stimulating hormone). It is especially useful for preparing proteins with  
CC more than five disulfide bridges, e.g. recombinant plasminogen activator  
CC (rPA). The technique is simple and does not require *in vitro* after-  
CC treatment, such as the removal of inclusion bodies, reduction or  
CC renaturation.

**SQ** Sequence 255 AA;

Query Match	76.8%	Score 977.5;	DB 3,	Length 255;
Best Local Similarity	78.9%	Pred. No. 3e-62;		
Matches 187;	Conservative 19;	Mismatches 26;	Indels 5;	Gaps 1.

Qy	1	VVKLQIESGGGLVYKPCGGSLKLTSCAAAGFFHSYVGMVNRPTPKRLREWVNTISSGGSYTX	60
Db	3	EVKIQESGGGLVQPGSGSRKLTSCAAAGFTTFSGGMHWKRAPEKGLRWYIISGSLTIY	62
Qy	61	PDVYKGRFTISRDNAKNTLYLQMSLSKEDTAMYYCARGNMGWYFDVWGCGTIVYVSSG	120
Db	63	ADTVYKGRFTISRDNPKNTLFLQMTSLRSEDITAMYYCARD-----YGAVYGGGTIVYVSSG	117
Qy	121	GGSGSGGGSGGGGSGNIELTQSPALMSAPGERVTMTCSASSIRIYYVQKPGGSPRL	180
Db	118	GGSGSGGGSGGGGSGDIELTQSPALMSAPGERVTMTCSASSSVRWMMWFOQSGTSPKRW	177
Qy	181	IYDPSNVAPGVPRFRSGSGSGTSYSLTINBMEAEADATYYCOEMSGYPTTPGGGRTL	237
Db	178	IYDTSKSSGVVPARFSGSGSGTSYSLTISMAEADATYYCOQMSNPLTFAGATL	234

## RESULT 4

ID AAB74199 standard; protein; 255 AA.

AC AAB74199,  
vv

DT 29-MAY-2001 (first entry)  
XX

DE PeLB-scFvOxazolone fusion protein.

**KM** molecular chaperone; **Pe1b** signal sequence; **scFvOxazon**

OS Unidentified  
xy

PN	EP1077262-A1.
XY	

PD 21-FEB-2001.  
VY

PF 24-JUL-2000; 2000EP-00115839.  
YY

PR 29-JUL-1999; 99EP-00114811.  
XY

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
XX

PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E,  
XX

DR WPI; 2001-246712/26.  
DR N-PSDB: AAF77806

XX	Producing natural
PT	

PT interferon, hormones or proteases that contain two or several cysteines  
PT linked by disulfide bridges comprises co-expression of a molecular  
PT chaperone.

PS Disclosure; Page 19; 35pp; English  
xy

CC The present invention relates to a method for production of a naturally  
CC folded eukaryotic protein containing two or more cysteines linked by  
CC disulfide bridges. The method comprises co-expression and secretion into

the periplasm of a molecular chaperone via an expression vector coding for the chaperone. The expression vector also encodes a signal sequence. The method is useful for producing a naturally folded eukaryotic protein, such as an antibody, antibody fragment, interferon, protein hormone or a protease containing two or several cysteines linked by disulfide bridges. The present sequence is a fusion protein composed of the PelB signal sequence and ScpVoxazolone. This sequence was used in the method of the present invention.

Sequence 255 AA;

Query Match	76.8%;	Score 977.5;	DB 4;	Length 255;
Best Local Similarity	78.9%;	Pred. No. 3e-62;		
Matches 187;	Conservative 19;	Mismatches 26;	Indels 5;	Gaps 1;

[illegible]

## RESULT 5

ID AAB70769 standard; protein; 255 AA.

AC AAB70769

DT 18-MAY-2001 (First entry)

DE Expression plasmid pUBS520-ScFvOx protein.

KM Chaperone protein; periplasm; antibody production; protein production;  
KM interferon production; protease production.  
...

Escherichia coli.

XX

2  
1  
1  
1  
2  
2  
2  
2

2000

XX 00 777 1 000 0075 00114011

[illegible]

XX  
EDT 2001-2003EE/21

DR N-PSDB; AAF61193.

PT	Preparatio
----	------------

PT from periplasm or medium.

XX

PS Disclosure; Page 20-21; 36pp; German.

CC This invention describes a novel method

CC Cys residues by culturing prokaryotic cells that contain an expression  
CC vector for (I) including a prokaryotic signal sequence at its N-terminus  
CC and a nucleic acid (II) that secretes a chaperone protein (III) into the  
CC periplasm. (I) is secreted into the periplasm or medium; the signal





PR	12-JUL-2000; 2000DE-01033750.
XX	
XX	(MPBC-) MPB COLOGNE GMBH.
PA	
XX	
PI	Duerling K, Brinkmann O;
XX	
DR	WPI; 2002-154868/20.
DR	N-PSDB; AAK98639.
XX	
PT	Imparting pathogen resistance to plants and animals, comprises using a
PT	polypeptide that binds to an oxazole-derived ketone, optionally expressed
XX	from nucleic acid.
XX	
PS	Example 3; Fig 1; 20pp; German.
XX	
CC	The present invention relates to the use of a polypeptide that binds a
CC	ketone derived from oxazole for generating pathogen resistance in an
CC	organism. This can be used to impart resistance to pathogens (bacteria,
CC	fungi or viruses) to a wide range of plants (e.g. cereals, sugar beet,
CC	tomacco etc.), humans, farm animals and pets. Exemplified are activities
CC	against Phytophthora infestans and Erwinia carotovora in potatoes and
CC	Staphylococcus aureus in mice. The present sequence is a bc-Fv antibody,
XX	which is capable of binding 2-phenyloxazol-5-one
XX	
AA	Sequence 241 AA;
XX	

Query Match	74.6%;	Score 949.5;	DB 5;	Length 241;
Best Local Similarity	77.5%;	Pred. No. 2.9e60;		
Matches 183;	Conservative 19;	Mismatches 29;	Indels 5;	Gaps 1;

QY 2 VKLQESGGGLVYKGGSGSLKLTSCAASGTFSSYCMSSVROTPIRLRLKMTLTSSGSGSYTYP 61

Db 4 VQLVESGGGLVYGGSGRKLSCAASGTFSSFGMHVRRQAPKGLKMTLVLTSSGSLTYTA 63

QY 62 DSYKGRFTISRDNKAKTLYLQMSLSKSEPTAMTYCARQNMGEWTFDWGGQGTITYVSSGG 121

64 DYKGRFTISRDNPKNTLFLQMTSLRSEPTAMTYCARD---YGAVVGQGTITYVSSGG 118

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QY      122  GSGSGSGSGSGSNIELTOSPAIMASPGERYMTCSASSSRYYIYQOKFGSSPRLI  181
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      119  GSGSGSGSGSGSDIELTGSALMASPGEXTMTCSASSSRYYMMNFQOKGSTPKRWI  178

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**OY**      182 YDTSNAPGVPRFRSSGGGTSYLTIINRHEAEDAATYYCQEWSGIPTYTGGGTKL 237  
||| :: ||||| : ||||| : |||||  
**D6**      179 YDTSKLSGVPARFSGSGGSVSLTIISNEAEDAATYYCCQWSSNPLTFGAGTKL 234

RESULT 10  
AAR32842  
ID AAR32842 standard; protein; 236 AA

XX	25-MAR-2003	(revised)
DT	19-JUN-1993	(first entry)
DT		

DE	VH NQ10/12.5-Vk NQ10/12.5 linked peptide sequences #2.
XX	
KW	Primer; human; immunoglobulin; Ig; variable region; VH

08	Synthetic.
XX	
KM	NQ2/12.4; NQ10/12.5.
05	

Key	Location/Qualifiers
FH	1. .115
FT	/label= VH NQ10/12.
FT	

Region	/note= "Linker peptide"
FT	130..236
FT	/label= Vkapppa_NQ10/12.5
FT	

XX WO9303151-A1.  
 PN  
 XX  
 PD 18-FEB-1993.  
 XX  
 PF 10-AUG-1992; 92WO-GB001483.  
 XX  
 PR 10-AUG-1991; 91GB-00017352.  
 PR 11-JUN-1992; 92GB-00012419.  
 XX  
 PA (MEDT-) MEDICAL RES COUNCIL.  
 XX  
 PI Embledon MJ, Gorochov G, Jones PT, Winter GP;  
 XX WPI; 1993-076508/09.  
 DR N-PSDB; AAQ37461.  
 DR

PT copies of 2 or more non-contiguous DNA sequences to facilitate analysis  
XX  
PS Disclosure; Fig 4; 72pp; English.

CC The sequences given in AAR32840-43 show the mature heavy chain VH domain  
CC and the VH light chain genes of the antihepatomyxolone hybridomas  
CC NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by in-  
CC cell PCR. The cDNA encoding these peptides was synthesised using forward  
CC primers annealing to the Ck gene and the JH segment, followed by assembly  
CC with linker primers, VH back primers based on the VH3 leader sequence and  
CC a forward Ck primer nested in respect to the primer used for cDNA. The  
CC assembled product within the cells is then amplified with nested primers  
CC annealing to the 5' end of the VH gene and the 3' end of the Jk segment.  
CC In-cell PCR may be used to determine gene linkage analysis, particularly  
CC for the cloning of gene combinations that are polymorphic within a  
CC population of cells, such as the rearranged genes for Ig or TCR V  
CC regions. (Updated on 25-MAR-2003 to correct PN field.)

SQ	Sequence 236	AA;
Query Match	74.5%	Score 947.5; DB 2; Length 236;

[illegible]

Db	62	DTVAGRFTISRDNPKNTLFLQMTSRSEDTAMYCARD-----YGAYWGQGTLLVTVSAGG	116
Oy	122	GGSGGGGGGGGSGNIELTOSPAINSASPGERVTMTCSASSIRIYIYQQRGSSPRLLI	181

Dy	182 YDTSNVAPGVPFRPSGGSGSTSYSLTINRMEADATYYCOEWSGYPTTFGGCTKL 237
Dz	117 GGS6GGGGSGSSQIVLTQSPALMSASPGEKVTMTCSASSSVRYMMWFQQSGTSPKRMI 176

Db 177 YDTSKLSGVPARFSGSGSTSLTSSMEADDAITYCQWSSNPITFGAGTKL 232

RESULT 11  
AAB20436  
ID AAB20436 standard; protein; 249 AA

AC	AAB20436;
XX	
DT	21-JUN-2001 (first entry)

DT	21-JUN-2001	(first entry)
XX		
DE	Anti-FIX/FIXa antibody 198/A1 scFv	

KM Factor IX; FIX, Factor IXa, FIXa, scFv; procoagulant;  
KM Factor VIII cofactor; blood coagulation disorder; haemophilia A  
KM haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse  
XX

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OS Mus musculus.
OS Synthetic.
OS Chimeric.
FH Key
FT Location/Qualifiers
FT 1..122
FT /label= VH
FT Region
FT 99..111
FT /label= CDR3
FT Peptide
FT 123..136
FT /label= Linker
FT 137..249
FT /label= VL
FT Misc-difference
FT 142
FT /note= "encoded by ACN"
FT Misc-difference
FT 224
FT /note= "encoded by GCN"
FT Region
FT 230..238
FT /label= CDR3
XX WO200119992-A2.
XX 22-MAR-2001.
XX 13-SEP-2000; 2000WO-EP008936.
XX 14-SEP-1999; 99AT-00001576.
XX (BAXT ) BAXTER AG.
XX Scheiflinger F, Kerschbaumer R, Falkner F, Dornier F;
XX WPI; 2001-290358/30.
XX N-PSDB; AAF30726.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
XX increasing amidolytic activity of factor IXa, and for treating blood
XX coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
XX Example 10; Fig 17; 138pp; English.
XX
XX The present sequence is that of a single chain Fv (scfv) derivative of
XX antibody 198/A1, comprising the heavy (VH) and light (VL) chain variable
XX regions of 198/A1 joined by an artificial, flexible linker peptide. The
XX scfv was obtained by PCR amplification of cDNAs for 198/A1 VH and VL
XX regions and cloning in vector pDAp2. 198/A1 is an example of anti-human
XX Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the invention.
XX Anti-FIX/FIXa and their derivatives, including scfv and CDR3 fragments,
XX have Factor VIIa (FVIIa) cofactor activity or FIXa activating activity.
XX Administration leads to an increase in the procoagulant activity of FIXa,
XX even in the presence of FVIIa inhibitors. This allows for rapid blood
XX coagulation even in the absence of FVIIa or FVIIa, and in the case of
XX FVIII inhibitor patients. The antibodies and derivatives are used in a
XX claimed pharmaceutical composition for treating patients with blood
XX coagulation disorders, especially haemophilia A and haemorrhagic
XX diathesis
XX
XX Sequence 249 AA;
SQ
Query March 73.6%; Score 936; DB 4; Length 249;
Best local Similarity 72.7%; Pred. No. 2.8e-59;
Matches 178; Conservative 26; Mismatches 33; Indels 8; Gaps 2;
QY 1 QVKLQESGGGLVKKPGSGSLKSCAASGFTFSSYGMWVQTPDKRLQEWATISSGGSYYY 60
DB 1 EVQIQESGGGLVKKPGSGSLKSCAASGFTFSSYGMWVQTPDKRLQEWATISSGGSYYY 60
QY 61 PDSVKGRTTISRDNKNTLYLQMSLKSSEDPMAYCAR--GNWEGWTFDVGQCTTATV 117
DB 61 PDSVKGRTTISRDNKNTLYLQMSLKSSEDPMAYCHCTREGGYYVNWYFDWAGATTLTV 120
QY 118 SSGGGSGGGSGGGSGGNIETQSAPAIMSAPGSEVMTTCASSSI-----RYIYVYQOK 172
DB 118 SSGGGSGGGSGGGSGGNIETQSAPAIMSAPGSEVMTTCASSSI-----RYIYVYQOK 172

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DB 121 SSGGGSGGGSGGGSGGDIETQSAPLAIVSLGQRATISCRASSEVDYSGKSFHWYQOK 180
QY 173 FGSSPRLIYDTSNVAPGVPPRFSGSGSGTSYSTLTIRMEADATYYCQWSGYPRTFG 232
DB 181 FGQPPKLIYRASNLSGIPARFSGSGSRDFTLTINPVADVATYYCQQSNEDPLTFG 240
QY 233 GGTKL 237
DB 241 AGTRL 245
RESULT 12
AAR68613
ID AAR68613 standard; protein; 240 AA.
XX
XX AAR68613;
XX
XX 25-MAR-2003 (revised)
XX 13-SEP-1995 (first entry)
XX
XX Single chain antibody (scfv) which binds to phenylloxazone.
XX
XX Genetic selection; ligand binding protein; cholera toxin; promoter;
XX detection; selection; beta galactosidase; lac; transmembrane domain;
XX regulatory domain; ds.
XX
XX Synthetic.
XX
XX DE4319296-A1.
XX
XX 15-DEC-1994.
XX
XX 10-JUN-1993; 93DE-04319296.
XX
XX 10-JUN-1993; 93DE-04319296.
XX
XX 10-JUN-1993; 93DE-04319296.
XX
XX (BEHW ) BEHRINGWERKE AG.
XX
XX Fritzt H, Hennecke F, Kolmar H;
XX
XX WPI; 1995-023689/04.
XX N-PSDB; AAQ80468.
XX
XX Genetic selection of ligand binding proteins in microorganisms - by
XX extracytoplasmic protein presentation, then use of ligand binding to
XX express a detectable or selectable function.
XX
XX Example 2.2; Fig 4; 25pp; German.
XX
XX Genetic selection in microorganisms, for ligand binding proteins (LBP)
XX comprises: extracytoplasmic presentation of LBP and; using the signal of
XX ligand binding (by signal transduction on the biosynthetic machinery of
XX the microorganisms) to express a detectable or selectable function.
XX Microorganisms for this process include a genetically stable
XX detection/selection and are transformed with a replicon encoding a fusion
XX protein consisting of the LBP, a transmembrane helix and regulatory
XX domain. The detection/selection function is expression of a beta-
XX galactosidase gene, integrated into the chromosome and under the control
XX of the ctx (cholera toxin) promoter. The transmembrane helix is taken
XX from the toxR gene. Four primers (AAQ80457-60) were used in the
XX construction of the plasmid pKTXscfv. The primers described in AAQ80457
XX -58 were used to amplify variable heavy chain sequence of the single
XX chain antibody NQ10.12.5 and those described in AAQ80459-60 were used to
XX amplify the corresponding light chain sequence from the same antibody.
XX The amplified sequences were cloned into the plasmid pKTXscfEI (See
XX AAQ80454-56 for details) to create a toxR-scfv fusion gene. This sequence
XX is the single chain antibody (scfv). (Updated on 25-MAR-2003 to correct
XX PN field.)
XX
XX Sequence 240 AA;
SQ
Query March 73.5%; Score 935.5; DB 2; Length 240;
Best local Similarity 76.3%; Pred. No. 2.9e-55;

```

Matches 180; Conservative 18; Mismatches 33; Indels 5; Gaps 1;

QY 2 VKLQSGGGLVPGKSLKSCAASGFTFSYGMWVROTPDKRLRWATISSGSSYTP 61  
 DB 6 VQLVLEGGGVQPGSKSLKSCAASGFTFSYGMWVROTPDKRLRWATISSGSSYTP 65  
 QY 62 DSVKGRFTISRDNKNTLYLQMSLKSDEDTAMYCARGNMGWYFDWGGTTVTSGG 121  
 DB 66 DTVKGRFTISRDNKNTLYLQMSLKSDEDTAMYCARGNMGWYFDWGGTTVTSGG 120  
 QY 122 GSGSGGGGGGSGSIETLQSPAINASAPGERVTWTCASASSIRITTYOQKPGSSPRLI 181  
 DB 121 GSGSGGGGGGSGSIETLQSPAINASAPGERVTWTCASASSIRITTYOQKPGSSPRLI 180  
 QY 182 YDTSNVAAGVPFPFGSGSGSTYSLTINRMEADDAATYYCOEMSGYPYTFGGGTKL 237  
 DB 181 YDTSKLSGGVPARFGSGSGSTYSLTINRMEADDAATYYCOEMSNPLTFAGTKL 236

RESULT 13  
 ID AAM90218 standard; protein; 556 AA.  
 AC AAM90218;  
 DT 10-MAY-1999 (first entry)  
 DE Bispesific tetraivalent antibody B1TAB1G10-B7-24H6.  
 KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;  
 KW T cell activation; inhibitor; graft versus host disease;  
 KW transplant rejection; allograft rejection; autoimmune disease; allergy;  
 KW therapy; human; bispesific tetraivalent antibody; B1Tab;  
 KW B1TAB1G10-B7-24H6.

OS Mus sp.  
 OS Homo sapiens.  
 OS Synthetic.  
 OS Chimeric.

XX  
 FT Key Location/Qualifiers  
 FT Region 1..120  
 FT Peptide /note= "VH region anti B7.2 Mab"  
 FT 121..135  
 FT /note= "(G4S3) flexible linker"  
 FT 136..248  
 FT /note= "VL region anti B7.2 Mab"  
 FT 249..259  
 FT /note= "human IgG3 hinge region"  
 FT 260..285  
 FT /note= "helix-turn-helix dimerisation domain"  
 FT 286..305  
 FT /note= "human IgG3 hinge domain"  
 FT 306..426  
 FT /note= "VH region anti B7.1 Mab"  
 FT 427..441  
 FT /note= "(G4S3) flexible linker"  
 FT 442..550  
 FT /note= "VL region anti B7.1 Mab"  
 FT 551..556  
 FT /note= "His6 tag"

XX  
 PN WO858965-A2.  
 PD 30-DEC-1998.  
 PF 22-JUN-1998; 98WO-EP003791.  
 PR 20-JUN-1997; 97EP-00870092.  
 XX (INNO-) INNOGENETICS NV.  
 PA  
 XX  
 PI Lorre K, Sablon E, Buysse M, Bosman A;

XX  
 DR WPI: 1999-105615/09.  
 DR N-PSDB; AAX01652.  
 XX  
 FT New molecules which bind B7.1 and B7.2 - useful to prevent and treat  
 PT immune diseases including allograft rejection.  
 XX  
 PS Example 7.1; Fig 18; 182pp; English.

XX This polypeptide comprises the bispesific tetraivalent antibody B1TAB1G10-B7-24H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2 anti B7.2 scFvs (tetravalency). One single B1Tab is a homodimer of 2 identical molecules, each containing both an anti B7.1 and anti B7.2 scFv (bispesificity). An anti-B7.1 and anti-B7.2 scFv are linked using a dimerisation domain (see AAM90219), which drives the homodimerisation of the molecule. DNA (see AAX01652) encoding the B1Tab has been constructed to allow expression of the B1Tab in transformed E. coli cells. The B1Tab cross-links, and/or cross-reacts, with the costimulatory molecules B7.1 and B7.2 that are expressed on the membrane of professional antigen-presenting cells, leading to the inhibition of antigen-specific T cell activation. The invention relates to such B7-binding molecules, methods for their production, and their use for treating or preventing diseases of the immune system, in particular graft rejection, graft versus host disease, allergy and autoimmune diseases (claimed).

SO Sequence 556 AA;

Query Match 73.3%; Score 932.5; DB 2; Length 556;  
 Best Local Similarity 74.5%; Pred. No. 1.2e-58;  
 Matches 178; Conservative 25; Mismatches 31; Indels 5; Gaps 2;

QY 1 QVKLQSGGGLVPGKSLKSCAASGFTFSYGMWVROTPDKRLRWATISSGSSYTP 60  
 DB 311 QVKLQSGGGLVPGKSLKSCAASGFTFSYGMWVROTPDKRLRWATISSGSSYTP 370  
 QY 61 PDSVKGRTISRDNKNTLYLQMSLKSDEDTAMYCARGNMGWYFDWGGTTVTSGG 120  
 DB 371 ADSVKGRTISRDNKNTLYLQMSLKSDEDTAMYCARGNMGWYFDWGGTTVTSGG 427  
 QY 121 GSGSGGGGGGSGSIETLQSPAINASAPGERVTWTCASASSIRITTYOQKPGSSPRLI 178  
 DB 428 GSGSGGGGGGSGSIETLQSPAINASAPGERVTWTCASASSIRITTYOQKPGSSPRLI 487  
 QY 179 LLIYDTSNVAAGVPFPFGSGSGSTYSLTINRMEADDAATYYCOEMSGYPYTFGGGTKL 237  
 DB 488 PWIYGTISNLAAGVPFPFGSGSGSTYSLTINRMEADDAATYYCOEMSNPLTFAGTKL 546

RESULT 14  
 ID AAM90217 standard; protein; 580 AA.  
 AC AAM90217;  
 DT 10-MAY-1999 (first entry)  
 DE Bispesific tetraivalent antibody B1TAB7-24-IG10H6.  
 KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;  
 KW T cell activation; inhibitor; graft versus host disease;  
 KW transplant rejection; allograft rejection; autoimmune disease; allergy;  
 KW therapy; human; bispesific tetraivalent antibody; B1Tab;  
 KW B1TAB7-24-IG10H6.

XX  
 PN Mus sp.  
 PD Homo sapiens.  
 PF Synthetic.  
 PR Chimeric.  
 XX  
 FT Key Location/Qualifiers  
 FT Peptide 1..24  
 FT /note= "pe1B signal peptide"  
 FT 25..138  
 FT Region



```

FT      /note= "VH region anti B7.1 Mab"
FT      139..153
FT      /note= "(G4S3) Flexible linker"
FT      154..262
FT      /note= "VL region anti B7.1 Mab"
FT      261
FT      /note= "encoded by CTR"
FT      263..273
FT      /note= "human IgG3 hinge region"
FT      274..308
FT      /note= "helix-turn-helix dimerisation domain"
FT      309..319
FT      /note= "human IgG3 hinge domain"
FT      320..446
FT      /note= "VH region anti B7.2 Mab"
FT      322..327
FT      /note= "codons for these amino acids are not present in
FT      the DNA sequence for B7.1MAB7-24-IG1-H6 provided in the
FT      specification"
FT      Peptide
FT      447..461
FT      /note= "(G4S3)flexible linker"
FT      462..574
FT      /note= "VL region anti B7.2 Mab"
FT      575..580
FT      /note= "His6 tag"
XX      W09858965-A2.
XX      30-DEC-1998.
XX      22-JUN-1998; 98WO-EP003791.
XX      20-JUN-1997; 97EP-00870092.
XX      (INNO-) INNOGENETICS NV.
XX      Lorre K, Sablon E, Buysse M, Boeman A;
XX      WPI; 1999-105615/09.
XX      DR N-PSDB; AAX01651.
XX      New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX      immune diseases including allograft rejection.
XX      Example 7.1; Fig 16; 182pp; English.
XX      This polypeptide comprises the bispecific tetravalent antibody B7.1MAB7-24
XX      -1G10H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2
XX      anti B7.2 scFvs (tetravalency). One single B7.1MAB is a homodimer of 2
XX      identical molecules, each containing both an anti B7.1 and anti B7.2 scFv
XX      (bispecificity). An anti-B7.1 and anti-B7.2 scFv are linked using a
XX      dimerisation domain (see AAW90219), which drives the homodimerisation of
XX      the molecule. DNA (see AAX01651) encoding the B7.1MAB has been constructed
XX      to allow expression of the B7.1MAB in transformed E. coli cells. The B7.1MAB
XX      cross-links, and/or cross-reacts, with the costimulatory molecules B7.1
XX      and B7.2 that are expressed on the membrane of professional antigen-
XX      presenting cells, leading to the inhibition of antigen- specific T cell
XX      activation. The invention relates to such B7-binding molecules, methods
XX      for their production, and their use for treating or preventing diseases
XX      of the immune system, in particular graft rejection, graft versus host
XX      disease, allergy and autoimmune diseases (claimed)
XX      Sequence 580 AA;
SQ
Query Match 73.3%; Score 932.5; DB 2; Length 580;
Best Local Similarity 74.5%; Pred. No. 1.2e-58;
Matches 178; Conservative 25; Mismatches 31; Indels 5; Gaps 2;
QY      1 QVQLQESGGGLVQPGGSLIKSCAASGFTFSYGMGSAWVQTPDKRLKLEWVATISGGSYYTY 60
DB      23 QVQLQESGGGLVQPGGSLIKSCAASGFTFSYGMGSAWVQTPDKRLKLEWVATISGGSYYTY 82
QY      61 PDSYKGRFTISRDNAKNTLYIQMDSLKSEDTAMYYCARAGNKGWYFDVWGQGTITVYSSG 120

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DB      83 ADSYKGRFTISRDNAKNTLYIQMDSLKSEDTAMYYCARAGNKGWYFDVWGQGTITVYSSG 139
QY      121 GGGSGGGSGGGSGGSGNIELTQSPALMSAPGERVMTSCASSSI--RYIYWOQKPGSSPR 178
DB      140 GGGSGGGSGGGSGGSDILTQSPSSMAASVGDRLVITTCVSRSRISSNLMHWYQKSGRTSPK 199
QY      179 LLIVDTNVAAPGVPRFRSSGSGTSTSLTNKREAEALATYYCQEMSGYPTTFGGGTL 237
DB      200 PWIVGTNLSAGVPSRSGSGSGTDTLTISMQPEDAATYYCOQWSSYPLTFQGGTKL 258

RESULT 15
AAU07497
ID      AAU07497 standard; protein; 252 AA.
AC      AAU07497;
XX      24-OCT-2001 (first entry)
DE      Synthetic antibody scFv (F8).
XX      Antimicrobial; antiviral; cytostatic; immunomodulatory; antibody;
XX      gene therapy; HIV; light chain; human immunodeficiency virus; tumour;
XX      metabolic disorder; immune disorder; auto-immune disorder; scFv (F8);
XX      cucumber mosaic virus.
XX      Synthetic.
XX      Key
XX      Location/Qualifiers
FT      1..125
FT      /label= VH
FT      /note= "Heavy chain variable region"
FT      126..140
FT      /label= Linker Peptide
FT      /note= "This peptide is specifically claimed in claim 17"
FT      141..252
FT      /label= VL
FT      /note= "light chain variable region"
XX      W0200149713-A2.
XX      12-JUL-2001.
XX      29-DEC-2000; 2000WO-IT000554.
XX      30-DEC-1999; 99IT-RM000803.
XX      (CEN) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.
XX      (CONS-) SOC CONSORTILE METAPONTUM AGRARIOS SRL.
XX      Benvenuto E, Franconi R, Desiderio A, Tavidoraki P;
XX      WPI; 2001-502555/55.
XX      DR N-PSDB; AAS11887.
XX      Peptides which are able to confer stability and solubility to an antibody
XX      comprising these peptides, useful for treating pathologies (e.g. tumor)
XX      associated with accumulation of a molecule inside or outside a human, or
XX      animal cell.
XX      Example 1; Page 81; 109pp; English.
XX      The invention relates to peptides which are able to confer stability and
XX      solubility to an antibody comprising these peptides. The peptides are
XX      especially H-FR1, H-FR2, H-FR3, H-FR4, L-FR1, L-FR2, L-FR3 or L-FR4
XX      present within a variable region of an antibody which makes the antibody
XX      soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to
XX      H-FR4 are present within the variable region of the heavy chain of an
XX      antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order (H
XX      -FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR4) and peptides
XX      having the sequences of L-FR1 to L-FR4 are present within the variable
XX      region of the light chain of an antibody, covalently linked to the L-

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CC CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(L-FR2)-(L-CDR2)-(L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and polynucleotides (e.g. by CC gene therapy) are useful for the manufacture of a medicament for the CC treatment of pathologies associated with accumulation of a molecule CC inside or outside a human, animal cell or plant cell. The pathologies are CC infectious (e.g. viral infections such as HIV, human immunodeficiency CC virus, infections), tumour, metabolic and immune (especially auto-immune) CC pathologies. The present sequence represents the synthetic antibody CC scFv(F8) which is used as a basis for constructing synthetic antibodies CC incorporating the peptides of the invention

XX  
SQ Sequence 252 AA;

Query Match 72.8%; Score 926.5; DB 4; Length 252;

Best Local Similarity 72.6%; Pred. No. 1,4e-58; Mismatches 31; Indels 11; Gaps 3;

Matches 180; Conservative 26; Mismatches 31; Indels 11; Gaps 3;

QY 1 QVRLQESGGGLVYPGSLKLSCAAGFTFSSYGMWVRQTPDKRLLEWVATISSGGSYTY 60  
Db 1 QVQLQESGGDLVQPGSLKLSCAAGFTFSSYGMWVRQTPDKRLLEWVATINSNGSTFY 60  
QY 61 PDSVKGFTISRDNKNTLYLQMSLSKSEPTAMYCA-RGNWEGW-----YFDVWGQGT 114  
Db 61 PDSVKGFTISRDNKNTLYLQMSLSKSEPTAMYCARRRNPYYGSRGYPDWGQGT 120  
QY 115 VTVSSGGGSGGSGGGSNIETOSPAIMSASPGERVMTCSASSI-----RYIYWY 169  
Db 121 VTVSSGGGSGGSGGGSIDIELTQSPALAVSLGQRATISCRASGVSDSYGNSFPMHW 180  
QY 170 QQKPGSSPRLLITDTSNVAPGVPPRFSGSGSGTSYSITINRMEADNATYYCOEWSGYPY 229  
Db 181 QQKPGQPPKLLIYRALNLESGIPARFSGSGSRITDFTLTINPEADVAITYCCQSNEDPW 240  
QY 230 TFGGGTKL 237  
Db 241 TFGGGTKL 248

Search completed: December 8, 2004, 17:16:45  
Job time : 169.707 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 8, 2004, 17:06:18 ; Search time 46.2439 Seconds  
(without alignments)  
493.111 Million cell updates/sec

Title: US-10-073-301a-9

Perfect score: 1272  
Sequence: 1 QVRLQESGGGLVPRGSLKL.....TTCQEMSGVPRYTGSGTKL 237

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.79:\*

1: PIR1:.\*  
2: PIR2:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	792.5	62.3	268	2 A56446	Ig heavy chain V r
2	697	54.8	249	2 S41374	single chain Fv an
3	631	49.6	233	2 JC5322	p53 specific singl
4	542	42.6	120	2 S55536	Ig heavy chain V r
5	535.5	42.1	119	2 P27888	Ig heavy chain V r
6	533	41.9	120	2 S55538	Ig heavy chain V r
7	533	41.9	120	2 S55537	Ig heavy chain V r
8	532	41.8	120	2 S55539	Ig heavy chain V r
9	532	41.8	548	2 S38864	Ig epsilon chain C
10	530	41.7	122	2 S78888	Ig heavy chain V r
11	522	41.0	254	2 B31790	Ig heavy chain V r
12	520.5	40.9	112	2 S26327	Ig heavy chain V r
13	520	40.9	117	2 PL0249	Ig heavy chain V r
14	514.5	40.4	121	2 I27887	Ig heavy chain V r
15	513	40.3	117	2 PL0252	Ig heavy chain V r
16	510.5	40.1	118	2 PH0096	Ig heavy chain V r
17	510.5	40.1	119	2 B27889	Ig heavy chain V r
18	510	40.1	152	2 B26471	Ig heavy chain pre
19	509.5	40.1	119	2 D27889	Ig heavy chain V r
20	509	40.0	124	2 C27888	Ig heavy chain V r
21	506.5	39.8	118	2 PH0097	Ig heavy chain V r
22	505.5	39.7	121	2 S55540	Ig heavy chain V r
23	505	39.7	138	2 S09258	Ig heavy chain V r
24	503.5	39.6	121	2 H27888	Ig heavy chain V r
25	501.5	39.4	123	2 G27888	Ig heavy chain V r
26	497.5	39.1	139	2 S38808	Ig heavy chain - m
27	495	38.9	119	2 B34353	anti-peptide Fab'
28	493.5	38.8	121	2 A27888	Ig heavy chain V r
29	493.5	38.8	121	2 D27888	Ig heavy chain V r

30	493	38.8	108	2 PH1006	Ig heavy chain V r
31	493	38.8	118	2 S20641	Ig heavy chain V r
32	492.5	38.7	112	2 A27889	Ig heavy chain V r
33	491	38.6	119	2 PH0098	Ig heavy chain V r
34	488.5	38.4	123	2 S63597	Ig heavy chain V r
35	483.5	38.0	120	2 S12953	Ig heavy chain V r
36	482.5	37.9	108	2 PH1010	Ig heavy chain V r
37	482.5	37.9	121	2 B27888	Ig heavy chain V r
38	482	37.9	138	2 S31666	Ig heavy chain V r
39	481	37.8	119	2 A43413	Ig heavy chain V r
40	480.5	37.8	121	2 H27887	Ig heavy chain V r
41	480.5	37.8	141	2 S31669	Ig heavy chain V r
42	479	37.7	119	2 D36005	Ig heavy chain V r
43	478	37.6	142	2 C34903	Ig heavy chain pre
44	477	37.5	111	2 PH1007	Ig heavy chain V r
45	476.5	37.5	147	2 I37780	Ig variable region

ALIGNMENTS

RESULT 1

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Jan-1996 #sequence #revision 19-Jan-1996 #text\_change 16-Aug-1996  
C:Accession: A56446  
R:Tang, P.M.; Folitz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995  
A:Title: A high affinity diroxin-binding protein displayed on M13 is functionally ident  
A:Reference number: A56446; MUID:9522583; PMID:7713873  
A:Accession: A56446  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-268 <TAN>  
A:Cross-references: GB:U20617  
C:Keywords: heterotetramer; immunoglobulin

Query Match 62.3%; Score 792.5; DB 2; Length 268;  
Best:Local Similarity 64.1%; Pred. No. 8.8e-48;  
Matches 152; Conservative 29; Mismatches 55; Indels 1; Gaps 1;

Qy	1 QVRLQESGGGLVPRGSLKLSCASGTFPSYGSWVRQTPDKLEWATISSGGSYYTY 60	
Db	3 QVRLQESGAEIVKPGASVKLSCTTSFNKIDTYMHWKQREGLGWIGRIAPANGITKY 62	
Qy	61 PDVYKGRFTISRDAKNTLYLQWMSLSKSEDTAMTYCARGNWEGVYFDVWGQTTVTVSSG 120	
Db	63 DPKFGKATTAADTSNTAYQLSLTSBEDTAIVYCA-SYLTLYENYWGQTTVTVSSG 121	
Qy	121 GGSGGGGGGGGGSNIELTQSPAIMSASPGERVTMTCSASSIRIYIYQKPSGSPRL 180	
Db	122 GGSGGGGDSGGGGDIETQSPAIMSASLGEKVTMSCRASSVNFIIYQKSPSLW 181	
Qy	181 IYDTSNAPGVPRFPFGSGGTSYSLTINMEADATYYCQEMSGVPRYTGSGTKL 237	
Db	182 VYTSHPGPVPRFPFGSGGNSYSLTISMEGDAATYYCQPTSPFTFGSGTKL 238	

RESULT 2

S41374  
single chain Fv antibody - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence #revision 06-Jan-1995 #text\_change 06-Jan-1995  
C:Accession: S41374  
R:Artsenko, O.; Weller, E.W.; Muentz, K.; Conrad, U.  
submitted to the EMBL Data Library, January 1994  
A:Description: Construction and functional characterization of a single chain Fv antio  
A:Reference number: S41374  
A:Accession: S41374  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-249 <ART>



C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 41.9%; Score 533; DB 2; Length 120;  
Best Local Similarity 85.0%; Pred. No. 3e-30;  
Matches 102; Conservative 8; Mismatches 8; Indels 2; Gaps 1;

Qy 2 VKLQESGGGLVPGGSLKLSCAASGFTFSSYGMWVRQTPDKRLKLEWATISSGGSYYTP 61  
Db 1 VKLQESGGGLVPGGSLKLSCAASGFTFSSYGMWVRQTPDKRLKLEWATISSGGSYYTP 60  
Qy 62 DSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCAR--GWMEGYFPVWGQTTVYSS 119  
Db 61 DSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCARLYDYDPVMDYWGQTTVYSS 120

## RESULT 7

55537 Ig heavy chain V region pe21 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S5537

R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995  
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using  
utations in the variable region genes.

A:Reference number: S55328; MUID:95239763; PMID:7536850

A:Accession: S5537

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <BOB>

A:Cross-references: EMBL:X8590; NID:9854306; PIDN:CAA57926.1; PID:9854307

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 41.9%; Score 533; DB 2; Length 120;  
Best Local Similarity 85.8%; Pred. No. 3e-30;  
Matches 103; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

Qy 2 VKLQESGGGLVPGGSLKLSCAASGFTFSSYGMWVRQTPDKRLKLEWATISSGGSYYTP 61  
Db 1 VKLQESGGGLVPGGSLKLSCAASGFTFSSYGMWVRQTPDKRLKLEWATISSGGSYYTP 60  
Qy 62 DSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCAR--GWMEGYFPVWGQTTVYSS 119  
Db 61 DSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCARLYDYDPVMDYWGQTTVYSS 120

## RESULT 8

55539 Ig heavy chain V region pe24 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S5539

R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using  
utations in the variable region genes.

A:Reference number: S55328; MUID:95239763; PMID:7536850

A:Accession: S5539

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <BOB>

A:Cross-references: EMBL:X8593; NID:9854312; PIDN:CAA57929.1; PID:9854313

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 41.8%; Score 532; DB 2; Length 120;  
Best Local Similarity 85.0%; Pred. No. 3.5e-30;  
Matches 102; Conservative 8; Mismatches 8; Indels 2; Gaps 1;

Qy 2 VKLQESGGGLVPGGSLKLSCAASGFTFSSYGMWVRQTPDKRLKLEWATISSGGSYYTP 61  
Db 1 VKLQESGGGLVPGGSLKLSCAASGFTFSSYGMWVRQTPDKRLKLEWATISSGGSYYTP 60

Qy 62 DSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCAR--GWMEGYFPVWGQTTVYSS 119  
Db 61 DSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCARLYDYDPVMDYWGQTTVYSS 120

## RESULT 9

53864

Ig epsilon chain C region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 24-May-2001

C:Accession: S3864

R:Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning of a

A:Reference number: S3864

A:Accession: S3864

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-548 <KIP>

A:Cross-references: EMBL:Z27397; NID:9416537; PIDN:CAA81768.1; PID:9440782

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:353-421/Domain: immunoglobulin homology <IMM>

Query Match 41.8%; Score 532; DB 2; Length 548;  
Best Local Similarity 68.3%; Pred. No. 1.7e-29;  
Matches 112; Conservative 6; Mismatches 22; Indels 24; Gaps 3;

Qy 1 QVKLQESGGGLVPGGSLKLSCAASGFTFSSYGMWVRQTPDKRLKLEWATISSGGSYYTP 60  
Db 1 QVKLQESGGGLVPGGSLKLSCAASGFTFSSYGMWVRQTPDKRLKLEWATISSGGSYYTP 60  
Qy 61 DSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCAR--GWMEGYFPVWGQTTVYSS 119  
Db 61 DSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCARQVSTWIRFAYWGQTLVYSSA 120  
Qy 120 GCGGSGGSGGSGGSGNIELTQSPAIMSAPG-----ERYTMC 157  
Db 121 G-----KTPPSVYPLAPSSAQTSMWTLGC 147

## RESULT 10

E2788

Ig heavy chain V region (H3-C6) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996

C:Accession: E2788

R:Catron, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhardt, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to a

A:Reference number: A91043; MUID:86300656; PMID:2427335

A:Accession: E2788

A:Molecule type: DNA

A:Residues: 1-122 <CAT>

A:Experimental source: strain Balb/c

A:Note: This sequence was isolated from a hybridoma protein that binds influenza virus

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 41.7%; Score 530; DB 2; Length 122;  
Best Local Similarity 85.1%; Pred. No. 4.9e-30;  
Matches 103; Conservative 5; Mismatches 9; Indels 4; Gaps 1;

Qy 2 VKLQESGGGLVPGGSLKLSCAASGFTFSSYGMWVRQTPDKRLKLEWATISSGGSYYTP 61  
Db 2 VKLQESGGGLVPGGSLKLSCAASGFTFSSYGMWVRQTPDKRLKLEWATISSGGSYYTP 61

Qy	62	DSVKRFTISRDNKNTLYLQMSLSKEPTAMYYCARG---	NWDEMGEPVWGOGTIVY	117
Dd	62	DSVKRFTISRDNKNTLYLQMSLSKEPTAMYYCTRQGEGRIDDYANDYMGGISVIY		121
Qy	118	S	118	
Dd	122	S	122	

```

RESULT 11
B31790
IG heavy chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-May-1997
C:Accession: B31790
R.:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an
A:Reference number: A92686; MUID:89034213; PMID:3182835
A:Accession: B31790
A:Molecule type: mRNA
A:Residues: 1-254 <SCH>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterodimer; immunoglobulin
C:15-98/Domain: immunoglobulin homology <IM>

```

	Query Match	41.0%;	Score 522;	DB 2;	Length 254;	
	Best Local Similarity	64.5%;	Pred. No. 3.7e-29;			
	Matches 107;	Conservative 13;	Mismatches 20;	Indels 26;	Gaps 3;	
Oy	1 QVKTLESGGGVKPCGSLKLSCAASGFPSISGXMSWVQTPDKRLREWATISSGGSYYY	60	:	:	:	:
Dd	1 EVOLVESGGDLVKPFGSLKLSCAASGFPSISGXMSWAQTPDKRLREWATISSGGGYIY	60	:	:	:	:
Oy	61 PDSVXGRFTISRDNAKNTLYLQMSLKSEDTAMNYCA-RGNWEGVPDVMGGGTIVTSS	119	:	:	:	:
Dd	61 PDSVXGRFTISRDNAKNTLYLQMSLKSEDSAMYCARERBYDENRGFAWGGTLVTYSA	120	:	:	:	:
Oy	120 GGGSGGGGSGGGGSNIELTOSPAIMASP-----GERVTMTC	157	:	:	:	:
Dd	121 A-----KTTAPSVYPPLAPVGXXDXDTGGSSVTLGC	149	:	:	:	:

```

RESULT 12
S26327
Ig heavy chain V region - mouse (Fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C:Accession: S26327
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:9134421; PMID:1908510
A:Accession: S26327
A:Molecule type: mRNA
A:Residues: 1-112 <STB>
A:Cross-references: EMBL:X59192
C:Superfamily: Immunoglobulin V region, immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
#9-91/Domain: immunoglobulin homology <IMM>

```

Query Match	40.9%	Score 520.5	DB 2	Length 112
Best Local Similarity	89.7%	Pred No. 2e-23		
Matches 102	Conservative 5	Mismatches 3	Indels 5	Gaps 3

  

QY	7	SGGGLVNRKGGSLKLSKCAASGFTFSYIGMSWVRQTPDKLELVANVATISGGGSYTYYPDSYXG	66
DB	1	SGGGIVNRKGGSLKLSKCAASGFTFSYIGMSWVRQTPDKLELVANVATISGGGS--TYYPDSYXG	59
QY	67	RFTISRDNAAKNTLYLQWMSLKSESDPAMYCYAR--GNMGKGVYFDVWGQGGTYTVSS	119
DB	60	RFTISRDNAAKNTLYLQWMSLKSESDPAMYCYARLNTY--NTEFDWGAGCTTVSS	112

RESULT 13  
PL0249  
I9 heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)  
C|Species: Mus musculus (house mouse)  
C|Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
A|Accession: PL0249  
R|Shomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J. Exp. Med. 171, 265-297, 1990  
A|Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
A|Reference number: PL0231; MUID:9011618; PMID:2104929  
A|Accession: PL0249  
A|Molecule type: mRNA  
A|Residues: 1-117 <SHD>  
C|Superfamily: immunoglobulin V region; immunoglobulin homology  
C|Keywords: heterotetramer; immunoglobulin  
F|1-30/Region: framework 1  
F|15-98/Domain: immunoglobulin homology <IMM>  
F|31-35/Region: complementarity-determining 1  
F|36-49/Region: framework 2  
F|50-66/Region: complementarity-determining 2  
F|67-98/Region: framework 3  
F|99-108/Region: complementarity-determining 3  
F|109-117/Region: framework 4

Query Match	40.9%	Score 520;	DB 2;	Length 117;
Best local similarity	83.8%	Pred. NO. 2.3e-29;		
Matches	98;	Conservative	7;	Mismatches 12;
			Indels	0; Gaps 0
QY	1 QYKIQESGGGLVKKGGSLKLSGASGFFSSYGMNWNQTPDKRLKLEWATISSGGSYTY	60		
Db	1 EVKLVESGGGLVKKGGSLKLSGASGFFSSYTMWQTPDKRLKLEWANSRRGGSTY	60		
QY	61 PDSVKGRTTISRDNAKNTLYLQMSLKSEDTAMYYCARGNMGWFDVWGQTTVY	117		
Db	61 PDSVKGRTTISRDNARNLTLYLQMSLRBEDDAVYYCARDDSHMFDFDWAGGTTVY	117		

RESULT 14  
I27887  
Ig heavy chain V region (H37-45) - mouse  
C|Species: Mus musculus (house mouse)  
C|Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #ext\_change 16-Aug-1996  
C|Accession: I27887  
R|Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A|Title: Structural and functional implications of a restricted antibody response to a  
A|Reference number: A91043; MUID:86300658; PMID:2427335  
A|Accession: I27887  
A|Molecule type: DNA  
A|Residues: 1-121 <CAT>  
A|Experimental source: strain Balb/c  
A|Note: this sequence was determined from the germ-line gene  
C|Comment: This chain was isolated from a hybridoma protein that binds influenza virus  
C|Superfamily: immunoglobulin V region; immunoglobulin homology  
C|Keywords: heterotrimer; immunoglobulin  
F|15-98/Domain: immunoglobulin homology <IMM>

[illegible]

## RESULT 15

PL0252  
 Ig heavy chain V region (anti-DNA, clones 2E3VH, 6B8VH, and 3G9VH) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
 C:Accession: PL0252; PL0251  
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Plasecky, D.; Marshak-Rochstein, A.  
 J. Exp. Med. 171, 265-297, 1990  
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
 A:Reference number: PL0231; MUID:90111618; PMID:2104919  
 A:Accession: PL0252  
 A:Molecule type: mRNA  
 A:Residues: 1-117 <SHL>  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-30/Region: framework 1  
 F:15-98/Domain: immunoglobulin homology <IMM>  
 F:31-35/Region: complementarity-determining 1  
 F:36-49/Region: framework 2  
 F:50-66/Region: complementarity-determining 2  
 F:67-98/Region: framework 3  
 F:99-108/Region: complementarity-determining 3  
 F:109-117/Region: framework 4

Query Match 40.3%; Score 513; DB 2; Length 117;  
 Best Local Similarity 82.9%; Pred. No. 6.9e-29;

Matches 97; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Qy	1	QVQLQESGGGLVPRGSGIKLSCAASGFTFSISYGMGVNROTDPDKRLRWVAITISGGSYTY	60
Db	1	EVKLVESGGGLVPRGSGIKLSCAASGFTFSISYGMGVNROTDPDKRLRWVAITISGGSYTY	60
Qy	61	PDSVKGRTTISRDNKNTLYLQMSLKSSEDPAHYCCARGNMGWYFDVWGQCTTVTV	117
Db	61	PDSVKGRTTISRDNKNTLYLQMSLKSSEDPAHYCCARGNMGWYFDVWGQCTTVTV	117

Search completed: December 8, 2004, 17:13:38  
 Job time : 47.2439 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 8, 2004, 17:06:18 ; Search time 6.29268 Seconds  
(without alignments)  
513.066 Million cell updates/sec

Title: US-10-073-301A-2

Perfect score: 45

Sequence: 1 IMDOVPPSV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23sep04:\*

1: geneseqp19908:\*\n2: geneseqp19908:\*\n3: geneseqp20008:\*\n4: geneseqp20018:\*\n5: geneseqp20028:\*\n6: geneseqp20038:\*\n7: geneseqp20038:\*\n8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	45	100.0	9 2 AAR84817	Aar84817 Modified
2	45	100.0	9 4 AAU28966	Aau28966 Modified
3	45	100.0	9 4 AAU72002	Aau72002 gp100 mel
4	45	100.0	9 4 AAU10221	Aau10221 Cancer ce
5	45	100.0	9 4 AAE05120	Aae05120 Modified
6	45	100.0	9 5 AAO17085	Aao17085 GP 100 an
7	45	100.0	9 5 AAE17297	Aae17297 gp100-mod
8	45	100.0	9 6 AAE36055	Aae36055 Tumour as
9	45	100.0	9 6 AAG79857	Aag79857 HLA-A2-re
10	45	100.0	9 6 AAE35575	Aae35575 Melanoma
11	45	100.0	9 6 ABJ19877	Abj19877 MHC bindi
12	45	100.0	9 6 ABU08668	Abu08668 Cancer ce
13	45	100.0	9 6 ADA89157	Ada89157 gp100-der
14	45	100.0	9 7 AAE38651	Aae38651 HLA-A2 re
15	45	100.0	9 7 ADB97733	Adb97733 Human gpi
16	45	100.0	17 4 AAU72227	Aau72227 gp100-der
17	45	100.0	17 4 AAU72226	Aau72226 gp100-der
18	45	100.0	17 4 AAU72231	Aau72231 gp100-der
19	45	100.0	20 4 AAU72232	Aau72232 gp100-der
20	45	100.0	20 4 AAU72224	Aau72224 gp100-der
21	45	100.0	20 4 AAU72229	Aau72229 gp100-der
22	45	100.0	20 5 AAE13455	Aae13455 Human gpi
23	45	100.0	20 5 AAE13456	Aae13456 Human gpi
24	45	100.0	25 4 AAU72228	Aau72228 gp100-der
25	45	100.0	25 4 AAU72232	Aau72232 gp100-der

26	45	100.0	30 4 AAB61648	Aab61648 gp100 pep
27	45	100.0	31 4 AAU72230	Aau72230 gp100-der
28	45	100.0	31 4 AAU72225	Aau72225 gp100-der
29	45	100.0	31 5 AAE13457	Aae13457 Human gpi
30	45	100.0	35 6 AAE35578	Aae35578 TA peptid
31	45	100.0	661 4 AAB97816	Aab97816 Modified
32	45	100.0	661 4 AAE05116	Aae05116 Modified
33	45	100.0	661 4 AAB98206	Aab98206 Human gpi
34	42	93.3	9 2 AAR84816	Aar84816 Modified
35	42	93.3	9 4 AAU28965	Aau28965 Modified
36	42	93.3	9 7 ADB97732	Adb97732 Human gpi
37	41	91.1	9 2 AAR84818	Aar84818 Modified
38	41	91.1	9 4 AAU28967	Aau28967 Modified
39	41	91.1	9 4 AAB97708	Aab97708 Avipox vi
40	41	91.1	9 4 AAB96098	Aab96098 Modified
41	41	91.1	9 7 ADB97734	Adb97734 Human gpi
42	39	86.7	9 2 AAR84210	Aar84210 gp100 mel
43	39	86.7	9 2 AAU70018	Aau70018 Melanoma-
44	39	86.7	9 2 AAU54599	Aau54599 Peptide 4
45	39	86.7	9 2 AAW78851	Aaw78851 PMEL 17 (

## ALIGNMENTS

RESULT 1  
AAR84817  
ID AAR84817 standard; peptide; 9 AA.  
XX  
XX AAR84817;  
XX AC  
DT 25-APR-1996 (first entry)  
XX  
DE Modified gp100 melanocyte-melanoma specific antigenic peptide G9-209-2M.  
XX  
KW MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma;  
KW metastatic melanoma; tumour-associated antigen; immunogenic peptide;  
KW diagnosis; prognosis; prophylaxis; therapy; vaccine.  
XX  
OS Synthetic.  
XX  
XX W09529193-A2.  
XX PN  
XX 02-NOV-1995.  
XX PD  
XX 21-APR-1995; 95WO-US005063.  
XX PP  
XX 22-APR-1994; 94US-00231565.  
XX PR 05-APR-1995; 95US-00417174.  
XX PA (USSH ) US SEC DEPT HEALTH.  
XX PI Kawakami Y, Rosenberg SA;  
XX DR WPI; 1995-382963/49.  
XX FT DNA encoding melanoma antigens recognised by T-lymphocytes - also  
XX PT vectors, host cells and antibodies, used to detect, treat and immunise  
XX PT animal against melanoma.  
XX  
XX Example 5; Page 107, 184pp; English.  
XX AAR84816-836 are G9-209 peptides modified to improve immunogenicity. G9-  
CC 209 is an immunogenic peptide based on the melanoma derived antigen,  
CC gp100 (see AAR84210). The peptides are used in medicaments for the  
CC treatment or prevention (by immunization) of melanoma. Antibodies against  
CC MART-1 and its immunogenic peptides may be used in the detection and  
CC isolation of MART-1 from a sample, the detection of which is indicative  
CC of a disease state (melanoma or metastatic melanoma)  
XX  
XX Sequence 9 AA;  
Query Match 100.0%; Score 45; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IMDQVPSV 9  
| | | | |  
Db 1 IMDQVPSV 9

## RESULT 2

AAU28966 standard; peptide; 9 AA.

AC AAU28966;

DT 18-DEC-2001 (first entry)

DE Modified gp100 G9-209 peptide #2.

XX Human; MART-1; immunogenic; melanoma antigen recognised by T lymphocyte;  
KM diagnostic; therapeutic; vaccine; melanoma; in vivo tumour recognition;  
KM in vivo tumour rejection.

XX Synthetic.

PN US6270778-B1.

PD 07-AUG-2001.

PF 12-MAR-1999; 99US-00267439.

XX 22-APR-1994; 94US-00231565.

PR 05-APR-1995; 95US-00417174.

PR 05-MAY-1998; 98US-00073138.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Kawakami Y, Rosenberg SA;

DR WPI; 2001-595403/67.

XX Immunogenic peptide useful in vaccines comprises specific amino acids of  
PT new melanoma antigen recognized by T lymphocytes.

XX Example 5; Col 55; 73pp; English.

CC The invention relates to a novel immunogenic peptide comprising 5-20  
CC contiguous amino acids of new melanoma antigen recognised by T

CC lymphocytes (MART-1). The peptide sequence contains at least one amino  
CC acid modification of MART-1. The peptide is used in diagnostic and

CC therapeutic methods as an immunogen or vaccine to prevent or treat  
CC melanoma, and for in vivo tumour recognition and rejection. AAU28888-  
CC AAU29008 represent MART-1 peptide amino acid sequences, and related  
CC sequences of the invention

XX Sequence 9 AA;

Query Match 100.0%; Score 45; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IMDQVPSV 9  
| | | | |  
Db 1 IMDQVPSV 9

## RESULT 3

AAU72002 standard; peptide; 9 AA.

AC AAU72002;

DT 26-FEB-2002 (first entry)

DE gp100 melanoma antigen #14.

XX Melanoma antigen; MART-1; MAGE-1; gp100; cytostatic; immune response;

KW Immunotherapeutic; heat shock protein; tyrosinase; BAG5; NYESO1; GM2;

KW tyrosinase related protein 1; tyrosinase related protein 2; vaccine;

XX javelin molecule; melanoma antigen recognised by T cells-1; human.

OS Homo sapiens.

XX WO200178655-A2.

PN 25-OCT-2001.

PF 17-APR-2001; 2001MO-US012449.

PR 17-APR-2000; 2000US-0197462P.

XX (HOUG/) HOUGHTON A.

PA (LIVI/) LIVINGSTON P.

PA (ALAM/) AL-AMOATI Q.

PA (MAYH/) MAYHEW M.

PA (HOEM/) HOE M.

XX Houghton A, Livingston P, Al-Awgati Q, Mayhew M, Hoe M;

DR WPI; 2001-663092/76.

XX Anti cancer vaccine for the treatment of melanoma comprises a heat shock  
PT protein and a melanoma antigen i.e. tyrosinase.

XX Claim 2; Page 11; 150pp; English.

CC The invention relates to a method of induction of an immune response,  
CC comprising administration of an immunotherapeutic composition, comprising

CC a heat shock protein, and a melanoma antigen, where the melanoma antigen  
CC is selected from tyrosinase, tyrosinase related protein 1, tyrosinase

CC related protein 2, gp 100, MAGE antigens, BAG5 antigens, NYESO1, MART  
CC antigens, GM2, antigenic portions and combinations of these. The melanoma

CC antigen is covalently bound to a javelin molecule, where the melanoma  
CC antigen bound to the javelin molecule is non-covalently bound to the heat

CC shock protein. The composition is useful for inducing an immune response  
CC for the treatment of melanoma. AAU71980-AAU72481 represent melanoma  
CC antigen peptides of the invention

XX Sequence 9 AA;

Query Match 100.0%; Score 45; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IMDQVPSV 9  
| | | | |  
Db 1 IMDQVPSV 9

AAU10221 standard; peptide; 9 AA.

AC AAU10221;

DT 27-FEB-2002 (first entry)

DE Cancer cell associated peptide G9-209-2M.

XX Human; cancer cell associated peptide; G9-209-2M; CTL;

KW single chain major histocompatibility complex class I; MHC;

XX human beta-2 microglobulin; cytotoxic T lymphocyte; cancer.

OS Homo sapiens.

XX WO200172768-A2.

PD 04-OCT-2001.  
 XX  
 PF 19-MAR-2001; 2001WO-II000260.  
 XX  
 PR 27-MAR-2000; 2000US-00534966.  
 XX  
 PA (TECR ) TECHNION RES & DEV FOUND LTD.  
 XX  
 PI Reiter Y;  
 XX  
 DR WPI; 2001-656911/75.  
 XX  
 PT New major histocompatibility complex (MHC) class I polypeptide, useful  
 PT for presenting antigenic peptides to cytotoxic T lymphocyte clones,  
 PT comprises beta-2 microglobulin covalently linked to MHC class I heavy  
 PT chain.  
 XX  
 PS Example 1; Page 27; 81pp; English.  
 XX  
 CC The invention relates to a recombinant single chain major  
 CC histocompatibility complex (MHC) class I polypeptide comprising an amino  
 CC acid sequence including a functional human beta-2 microglobulin  
 CC (in)directly covalently linked to a functional human MHC class I heavy  
 CC chain and the nucleic acids encoding it. The recombinant MHC polypeptide  
 CC is used in a method for generating large quantities of pure single  
 CC chain MHC class I polypeptides, which is useful in monomeric or  
 CC multimeric forms to present antigenic peptides to cytotoxic T lymphocyte  
 CC (CTL) clones. The present sequence is a cancer cell associated peptide  
 CC which can bind MHC in an experiment demonstrating the production of the  
 CC recombinant MHC complexes  
 XX  
 SQ Sequence 9 AA;  
 XX  
 Query Match 100.0%; Score 45; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IMPDVPFSV 9  
 DB 1 IMPDVPFSV 9  
 XX  
 RESULT 5  
 ID AAE05120 standard; peptide; 9 AA.  
 XX  
 AC AAE05120;  
 XX  
 DT 18-SEP-2001 (first entry)  
 XX  
 DE Modified tumour-associated antigen, GP100 peptide, CIP 572.  
 XX  
 KM Tumour-associated antigen; TAA; GP100 antigen; cytostatic; gene therapy;  
 KM immune response; tetanus toxoid; TT; diphtheria toxoid; DT; prophylactic;  
 KM vaccine; cancer; therapeutic.  
 XX  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT Misc-difference 2 /note= "Wild type Thr substituted with Met"  
 XX  
 PN WO200149317-A2.  
 XX  
 PD 12-JUL-2001.  
 XX  
 PF 05-JAN-2001; 2001WO-CA000005.  
 XX  
 PR 05-JAN-2000; 2000US-0174587P.  
 XX  
 PA (AVER ) AVENTIS PASTEUR LTD.  
 XX  
 PI Entage P, Barber BH, Sambhara S, Sia CDV;

XX  
 DR WPI; 2001-441790/47.  
 XX  
 PT Enhancing immune response to antigen such as tumor antigen for treating  
 PT cancer in an animal involves administering an inducing agent to the  
 PT animal followed by administering inducing agent-antigen mixture.  
 XX  
 PS Example 1; Page 28; 62pp; English.  
 XX  
 CC The invention relates to a method of enhancing an immune response against  
 CC tumour-associated antigens (TAAs), such as GP100 and carcinoembryonic  
 CC antigen (CEA) in an animal. The method involves priming of the animal  
 CC with an inducing agent such as tetanus toxoid (TT) or diphtheria toxoid  
 CC (DT), subsequently followed by administration of an inducing agent-  
 CC antigen mixture. The method provides the enhancement or augmentation of  
 CC the immune response to the antigen and/or improves a vaccination protocol  
 CC by allowing use of less antigen. The immunisation of the animal with  
 CC tumour-associated antigen is useful for the prophylactic or therapeutic  
 CC treatment of cancer. The present sequence is modified tumour-associated  
 CC antigen, GP100 peptide fragment related to the invention  
 XX  
 SQ Sequence 9 AA;  
 XX  
 Query Match 100.0%; Score 45; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IMPDVPFSV 9  
 DB 1 IMPDVPFSV 9  
 XX  
 RESULT 6  
 ID AAO17085 standard; peptide; 9 AA.  
 XX  
 AC AAO17085;  
 XX  
 DT 06-JUN-2002 (first entry)  
 XX  
 DE Gp 100 analogue antigen SEQ ID NO: 5.  
 XX  
 KM Cryopreserved mature dendritic cell; antigen; vaccine; cytostatic;  
 KM virucide; cancer; hepatitis B virus.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200216560-A1.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 24-AUG-2001; 2001WO-EP009790.  
 XX  
 PR 24-AUG-2000; 2000DE-01041515.  
 XX  
 PA (SCHU/) SCHULER G.  
 XX  
 PI Schuler G, Schuler-Thurner B;  
 XX  
 DR WPI; 2002-292062/33.  
 XX  
 PT Preparation of cryopreserved, mature dendritic cells, useful in vaccines,  
 PT comprises culturing immature cells on medium containing cocktail of  
 PT maturation factors, then freezing.  
 XX  
 PS Disclosure; Fig 28; 87pp; German.  
 XX  
 CC The present invention relates to a method for the preparation of ready-  
 CC for-use, cryopreserved, mature dendritic cells comprising growing  
 CC immature dendritic cells in a culture medium that includes a 'maturing  
 CC cocktail' of one or more maturation stimuli and freezing the resulting  
 CC matured cells in a freezing medium that does not contain heterologous  
 CC serum. When loaded with antigens, the dendritic cells can be used as

CC vaccines, e.g. against tumours and hepatitis B virus. The present  
CC sequence is an antigen described in the invention  
XX

Sequence 9 AA;

Query Match 100.0%; Score 45; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IMDQVPSV 9  
| | | | |  
| | | | |  
DB 1 IMDQVPSV 9

RESULT 7  
AAE17297  
ID AAE17297 standard; peptide; 9 AA.

AAE17297;

18-APR-2002 (first entry)

gpl100-modified peptide.

Artificial antigen presenting cell; AAPC; beta2-microglobulin;  
human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
cytotoxic T lymphocyte; CTL; T cell-specific antigen; TCA; antitumour;  
immune response; cancer.

Synthetic.

WO200194944-A2.

13-DEC-2001.

01-JUN-2001; 2001WO-US017981.

02-JUN-2000; 2000US-0209157P.

(SLOK ) SLOAN KETTERING INST CANCER RES.

Sadelain M, Latouche J;

WPI; 2002-139667/18.

Artificial antigen presenting cells for activating T lymphocytes,  
comprises eukaryotic cell expressing antigen presenting complex having  
beta2-microglobulin, exogenous accessory molecule, human leukocyte  
antigen molecule and protein.

Example 7; Page 29; 75pp; English.

The present invention relates to an artificial antigen presenting cell  
(AAPC) comprising a eukaryotic cell expressing an antigen presenting  
complex comprising beta2-microglobulin, an exogenous accessory molecule,  
a human leukocyte antigen, HLA (major histocompatibility complex, MHC)  
molecule of a single type and a protein that is processed intracellularly  
to produce an exogenous T cell-specific epitope. The invention also  
relates to methods for activation of T lymphocytes. The method is also  
useful for identifying within a test population of cytotoxic T  
lymphocytes (CTLs), CTLs specifically activated against a known T-cell  
specific antigen (TCA), which is useful for diagnostic purposes. AAPC is  
also useful for activating CTLs, by contacting AAPC with a suitable  
population of T lymphocytes under conditions suitable for the activation  
and isolating the activated CTLs. AAPC is further useful for the  
investigation of primary T cell activation and diagnostic applications  
here primary T cell activation allow discovery of antigens and accessory  
molecules, and diagnostic applications include cell-based assays for  
quantifying immune response in normal, infected or treated (vaccinated)  
patients. Composition comprising AAPC or activated T cells produced by  
utilising AAPC is useful for eliciting an antitumour response. The  
invention is used for the treatment of cancer. The present sequence is gp  
-100 modified peptide used in the exemplification of the invention

XX  
Sequence 9 AA;

Query Match 100.0%; Score 45; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IMDQVPSV 9  
| | | | |  
| | | | |  
DB 1 IMDQVPSV 9

RESULT 8  
AAE36055  
ID AAE36055 standard; peptide; 9 AA.

AAE36055;

26-JUN-2003 (first entry)

Tumour associated HLA-A2-restricted peptide, G9-209-2M.

Major histocompatibility complex; MHC; immune deception; cytostatic;  
therapy; cytotoxic T cell; immunostimulant; cancer.

Unidentified.

WO2002102299-A2.

27-DEC-2002.

18-JUN-2002; 2002WO-IL000478.

19-JUN-2001; 2001US-0298915P.

29-MAR-2002; 2002US-0010851L.

(TECR ) TECHNION RES & DEV FOUND LTD.

Reiter Y, Lev A;

WPI; 2003-210086/20.

New immuno-molecules comprising a soluble human major histocompatibility  
complex class I effector domain and a targeting domain linked to the  
effector domain, useful for immune deception, particularly in treating  
cancer.

Example; Page 50; 51pp; English.

The invention relates to immuno-molecules comprising a soluble human  
major histocompatibility complex (MHC) class I effector domain and a  
targeting domain linked to the effector domain, useful for immune  
deception. The invention also relates to methods for immune deception.  
The method is useful for producing an immunomolecule, and selectively  
killing a cell in a patient. The immuno-molecules are useful for immune  
deception, particularly treating cancer. The immuno-molecules and methods  
are useful for recruiting active cytotoxic T cells for tumour killing via  
cancer-specific antibody or ligand guided targeting of single-chain MHC-  
peptide complexes. The present sequence is a tumour associated HLA-A2-  
restricted peptide used to illustrate the method of the invention

Sequence 9 AA;

Query Match 100.0%; Score 45; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IMDQVPSV 9  
| | | | |  
| | | | |  
DB 1 IMDQVPSV 9

RESULT 9

AA679857  
ID AAG79857 standard; peptide; 9 AA.  
XX  
AC AAG79857;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE HLA-A2-restricted epitope of the gp100 melanoma antigen.  
XX  
KM Eptope; dendritic cell; tumour antigen-specific; CD8+ human cell clone;  
KM M15; HLA-A2-restricted epitope; gp100 melanoma antigen; M99;  
KM HLA-B7-restricted CD8+ CTL clone; carcinoembryonic antigen; cancer;  
KM haematological cancer; neurological cancer; melanoma; breast cancer;  
KM lung cancer; head; neck; gastrointestinal cancer; genitourinary cancer;  
KM bone cancer; vascular cancer; infection; influenza virus; HIV;  
KM M. tuberculosis; P. falciparum.  
XX  
OS Homo sapiens.  
XX  
PN WO200286083-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 22-APR-2002; 2002WO-US012733.  
XX  
PR 20-APR-2001; 2001US-0285137P.  
XX  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.  
XX  
PI Chen L, Strome SE;  
XX  
DR WPI; 2003-067637/06.  
XX  
PT Enhancing T cell responsiveness in a mammal, useful for treating cancer  
PT or other infections, comprises administering to the subject a compound  
PT comprising an agent that interferes with an interaction between B7-H1 and  
PT a T cell.  
XX  
XX Example 1; Page 31; 55pp; English.  
XX  
PS The sequences given in AAG79857-58 are epitopes which were used to  
CC stimulate dendritic cells to generate tumour antigen-specific CD8+ human  
CC cell clones. M15 is a human CD8+ CTL clone that specifically recognises  
CC an HLA-A2-restricted epitope of the gp100 melanoma antigen. M99 is an HLA  
CC -B7-restricted CD8+ CTL clone which recognises an epitope p  
CC carcinoembryonic antigen. The human T cell clones which are generated  
CC were used in the method of the invention for treating cancer, such as  
CC haematological cancer, neurological cancer, melanoma, breast cancer, lung  
CC cancer, head and neck cancer, gastrointestinal cancer, genitourinary  
CC cancer, bone cancer or vascular cancer, or infections by influenza virus,  
CC HIV, M. tuberculosis, or P. falciparum  
XX  
SQ Sequence 9 AA;  
XX  
Query March 100.0%; Score 45; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;  
XX  
QY 1 IMDOVPFSV 9  
XX  
DB 1 IMDOVPFSV 9

KM Fusion agent; immunogenic; proliferative disease; infectious disease;  
KM cancer; therapy; vaccine; melanoma; Trojan antigen; TA; epitope.  
XX  
OS Unidentified.  
XX  
XX WO200294994-A2.  
XX  
XX 28-NOV-2002.  
XX  
PD 20-MAY-2002; 2002WO-US015992.  
XX  
PF 18-MAY-2001; 2001US-0291874P.  
XX  
PR (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.  
XX  
PA Cells E;  
XX  
PI WPI; 2003-140367/13.  
XX  
DR Fusion agent useful for preventing and treating an infectious disease, or  
XX a proliferative disease, such as cancer, comprises a transport domain,  
XX two cleavage sites, a peptide epitope and a biologically active agent.  
XX  
PS Example 1; Page 37; 72pp; English.  
XX  
CC The invention relates to a fusion agent (Trojan antigen; TA) comprising a  
CC transport domain, two cleavage sites, a peptide epitope recognised by an  
CC antigen-specific receptor on an effector T-lymphocyte precursor cell and  
CC a biologically active agent, where there is a cleavage site between the  
CC peptide epitope and the biologically active agent and between each  
CC biologically active agent. The fusion agent is used to make a cell  
CC immunogenic or antigenic. It is also useful for preventing and treating  
CC an infectious disease such as viral, bacterial, protozoal, fungal or  
CC yeast disease, or proliferative disease such as cancer (e.g. melanoma,  
CC neural tissue, gastrointestinal, breast, lung, ovarian, testicular,  
CC prostate, cervical, bladder, vaginal, liver, renal, bone, haematological  
CC or vascular tissue cancer). The invention is used as vaccines. The  
CC present sequence is melanoma gp100 epitope. This peptide is used in the  
CC exemplification of the invention  
XX  
SQ Sequence 9 AA;  
XX  
Query March 100.0%; Score 45; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;  
XX  
QY 1 IMDOVPFSV 9  
XX  
DB 1 IMDOVPFSV 9

RESULT 11  
ABJ19877  
ID ABJ19877 standard; peptide; 9 AA.  
XX  
AC ABJ19877;  
XX  
DT 10-APR-2003 (first entry)  
XX  
DE MHC binding peptide SEQ ID No 42.  
XX  
XX Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;  
KM antiinflammatory; major histocompatibility complex; MHC;  
KM autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;  
KM rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;  
KM inflammation; gene therapy; MHC binding peptide.  
XX  
XX Synthetic.  
XX  
OS WO200294981-A2.  
XX  
PN 28-NOV-2002.  
XX  
PD

PF 16-MAY-2002; 2002WO-IT000383.  
XX  
PR 16-MAY-2001; 2001US-0290958P.  
PR 29-MAY-2001; 2001US-00865548.  
XX  
PA (TECR ) TECHNION RES & DEV FOUND LTD.  
PI Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;  
XX WPI; 2003-210043/20.  
XX  
DR  
XX  
XX Identifying peptides that are capable of binding to major  
PT histocompatibility complex (MHC) molecules of a particular haplotype by  
PT analyzing peptides bound to the soluble and secreted form of the MHC  
PT molecules of the particular haplotype.  
XX  
XX Example; Page 156; 238pp; English.  
XX  
XX The invention relates to a novel method for identifying peptides  
CC originating from a particular cell type, which are capable of binding to  
CC major histocompatibility complex (MHC) molecules of a particular  
CC haplotype. The method comprises analysing peptides bound to the soluble  
CC and secreted form of the MHC molecules of the particular haplotype. The  
CC method is useful for identifying peptides for treating an autoimmune  
CC disease, such as T or B cell and/or allergic disease or condition,  
CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,  
CC e.g. Alzheimer's disease, or diseases associated with inflammation. The  
CC sequences of the invention may be used in a gene therapy application.  
CC This sequence represents a peptide relating to the method for identifying  
CC MHC binding peptides of the invention  
XX  
SQ Sequence 9 AA;  
XX  
XX  
XX Query Match 100.0%; Score 45; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 IMDQVPSV 9  
Db 1 IMDQVPSV 9  
XX  
XX  
XX RESULT 12  
ABU08668  
ID ABU08668 standard; peptide; 9 AA.  
XX  
AC ABU08668;  
XX  
XX 10-JUN-2003 (first entry)  
XX  
DE Cancer cell associated peptide G9-209-2M.  
XX  
XX Chimeric polypeptide; antigenic peptide; MHC class I;  
XX major histocompatibility complex class I; beta-2 microglobulin;  
XX MHC class I heavy chain; single chain MHC class I;  
XX CTL; cytotoxic T-lymphocyte; MHC binding T cell epitope;  
XX Primary CTL induction; melanoma antigen gp100; cancer; G9-209-2M.  
XX  
OS Synthetic.  
XX  
XX US2003003535-A1.  
XX  
XX 02-JAN-2003.  
XX  
XX 13-FEB-2002; 2002US-00073300.  
XX  
XX 27-MAR-2000; 2000US-00534966.  
XX  
XX (TECR ) TECHNION RES & DEV FOUND LTD.  
XX  
XX Reiter Y;  
XX  
XX WPI; 2003-352830/33.

XX  
XX New chimeric polypeptide useful for generating antibodies, comprises an  
PT antigenic peptide that binds a human major histocompatibility complex  
PT (MHC) class I, a human beta-2 microglobulin and a human MHC class I heavy  
PT chain.  
XX  
XX Example 1; Page 9; 37pp; English.  
XX  
XX The invention describes a chimeric polypeptide (I) comprising an  
CC antigenic peptide capable of binding a human major histocompatibility  
CC complex (MHC) class I, a functional human beta-2 microglobulin and a  
CC functional human MHC class I heavy chain. The chimeric polypeptide is  
CC useful in generating large quantities of pure single chain MHC class I  
CC polypeptides which can be used in monomeric or multimeric form to present  
CC antigenic peptides to cytotoxic T-lymphocyte (CTL) clones. They may also  
CC be used in rapid, sensitive and reliable MHC peptide binding assay to  
CC identify high affinity MHC binding T cell epitopes, in vitro primary  
CC CTL induction studies to define those peptides that are immunogenic, and  
CC to generate antibodies. This is the amino acid sequence of a cancer cell  
CC associated peptide derived from melanoma antigen gp100 and used for major  
CC histocompatibility (MHC) binding  
XX  
SQ Sequence 9 AA;  
XX  
XX  
XX Query Match 100.0%; Score 45; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 IMDQVPSV 9  
Db 1 IMDQVPSV 9  
XX  
XX  
XX RESULT 13  
ADA89157  
ID ADA89157 standard; peptide; 9 AA.  
XX  
XX ADA89157;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
DE Gp100-derived peptide G9-209 SEQ ID NO:1.  
XX  
XX Immunoglobulin; Ig; heavy chain variable domain;  
XX light chain variable domain; major histocompatibility complex; MHC;  
XX gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;  
XX cancer; gene; ds.  
XX  
XX Synthetic.  
XX  
XX Homo sapiens.  
XX  
XX WO2003070752-A2.  
XX  
XX 28-AUG-2003.  
XX  
XX 20-FEB-2003; 2003WO-US005128.  
XX  
XX 20-FEB-2002; 2002US-0358994P.  
XX  
XX (DYAX-) DYAX CORP.  
XX (TECR ) TECHNION RES & DEV FOUND LTD.  
XX  
XX Hoogenboom HRDM, Reiter Y;  
XX  
XX WPI; 2003-663847/62.  
XX  
XX  
XX New protein comprising an immunoglobulin heavy chain variable (VH) domain  
PT and an immunoglobulin light chain variable (VL) domain, useful for  
PT preparing a composition for treating or preventing a cancerous disorder.  
XX  
XX Claim 4; Page 137; 224pp; English.  
XX  
XX The present invention describes a protein comprising an immunoglobulin

CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)  
CC domain. The protein binds a complex comprising a major histocompatibility  
CC complex (MHC) and a peptide, does not substantially bind the MHC in the  
CC absence of the bound peptide, and does not substantially bind the peptide  
CC in the absence of the MHC. The peptide is a peptide fragment of gp100,  
CC MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition  
CC comprising the novel protein and a carrier; (2) a cytotoxic T cell  
CC comprising one or more nucleic acids for expressing the Ig that binds a  
CC complex having an MHC and a peptide, does not substantially bind the MHC  
CC in the absence of the bound peptide, and does not substantially bind the  
CC peptide in the absence of the MHC; (3) an isolated nucleic acid  
CC comprising a first segment that encodes the Ig variable domain; (4) a  
CC host cell comprising heterologous nucleic acid sequences that encodes the  
CC novel protein; (5) a transgenic animal whose genome includes heterologous  
CC nucleic acid sequences that encode the protein; (6) identifying the  
CC protein that specifically binds the MHC-peptide complex; (7) expressing  
CC an antigen-binding protein; (8) ablating or killing a target cell that  
CC displays a peptide on a surface MHC molecule; (9) treating or preventing  
CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide  
CC complex in a sample. A protein of the invention has cytostatic activity,  
CC and can be used in gene therapy. The protein is useful for preparing a  
CC composition for treating or preventing a cancerous disorder. The present  
CC sequence represents a gp100-derived peptide, which is used in the  
CC exemplification of the present invention.

SQ Sequence 9 AA;

Query Match

Best Local Similarity 100.0%; Score 45; DB 6; Length 9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 1 IMDQVPSV 9  
| | | | | | | | |  
Db 1 IMDQVPSV 9

RESULT 14

ID AAE38651 standard; peptide; 9 AA.

AC AAE38651;

DT 04-DEC-2003 (first entry)

DE HLA-A2 restricted peptide, gp100 (209).

XX Major histocompatibility complex; MHC; HLA-restricted antigen; cancer;

KW viral infection; autoimmune disease; gene therapy; cytostatic; virucide;

KW immunomodulator.

XX Unidentified.

OS WO2003068201-A2.

XX 21-AUG-2003.

PF 11-FEB-2003; 2003WO-IL000105.

PR 13-FEB-2002; 2002US-00073301.

XX (TECR ) TECHNION RES &amp; DEV FOUND LTD.

PI Relter Y, Denkerberg G;

XX WPI; 2003-689603/65.

DR New isolated molecule comprising an antibody that binds with a human

PT major histocompatibility complex (MHC) class I being complexed with a HLA

PT autoimmune disease.

XX Example; Page 10; 81pp; English.

CC The invention relates to an isolated molecule comprising an antibody  
CC specifically bindable with a binding affinity below 20 nanomolar to a  
CC human major histocompatibility complex (MHC) class I being complexed with  
CC a HLA-restricted antigen. The molecule, antibodies, and methods are  
CC useful for treating cancer, viral infection and an autoimmune disease.  
CC The invention is useful in gene therapy. The present sequence is HLA-A2  
CC restricted peptide

SQ Sequence 9 AA;

Query Match

Best Local Similarity 100.0%; Score 45; DB 7; Length 9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 1 IMDQVPSV 9  
| | | | | | | | |  
Db 1 IMDQVPSV 9

RESULT 15

ID ADB97733 standard; peptide; 9 AA.

AC ADB97733;

DT 04-DEC-2003 (first entry)

DE Human gp100 antigenic peptide #12 analogue #2.

XX Human; melanoma antigen recognised by T-lymphocytes; MART-1; melanoma;

KW skin cancer; T lymphocyte; cytostatic; gene therapy; vaccine; antigen;

KW major histocompatibility complex; MHC; human leukocyte antigen; HLA-A2;

KW tumour infiltrating lymphocyte; mutant; melanin.

XX Synthetic.

OS Homo sapiens.

XX US2003144482-A1.

XX 31-JUL-2003.

PF 03-JUL-2001; 2001US-00898860.

XX 22-APR-1994; 94US-00231565.

PR 12-MAR-1999; 99US-00267439.

XX (KAWA/) KAWAKAMI Y.

PA (ROSE/) ROSENBERG S A.

XX Kawakami Y, Rosenberg SA;

PI WPI; 2003-75536/71.

DR New immunogenic peptides derived from melanoma antigens recognized by T-

PT lymphocytes or from gp100, useful for preventing or treating melanoma.

XX Example 5; Page 31; 77pp; English.

CC The invention relates to an immunogenic peptide having contiguous amino  
CC acids derived from the sequence of melanoma antigens recognised by T-  
CC lymphocytes (MART-1) or gp100. The MART-1 sequence appears as ADB97651,  
CC and the gp100 (differing by 1 amino acid from the previously published  
CC gp100 (ADB97770) appears as ADB97676. Also included are a pharmaceutical  
CC composition (comprising the above peptide and an excipient, diluent or  
CC carrier), a vaccine for immunising a mammal (comprising the above peptide  
CC in a carrier), preventing or treating melanoma (comprising administering  
CC the above composition to a mammal in an amount to stimulate the  
CC production of protective antibodies or immune cells), a purified and  
CC isolated nucleic acid sequence encoding the above peptide, a recombinant  
CC expression vector comprising at least one nucleic acid sequence cited  
CC above, a host organism transformed or transfected with the vector  
CC (expressing the peptide) and antibodies reactive with the above  
CC immunogenic peptide. The peptide sequence contains at least one amino

CC acid modification (amino acid substitution) of the MART-1 or gp100  
CC sequence to enhance binding of the peptide to a Major Histocompatibility  
CC Complex (MHC) molecule. The peptide is recognised by Human Leukocyte  
CC Antigen (HLA)-A2 restricted tumour infiltrating lymphocytes. The  
CC composition and methods are useful in preventing or treating melanoma and  
CC skin cancer. The present sequence represents a modified melanoma  
CC antigenic peptide of the invention.  
XX

SQ Sequence 9 AA;

Query Match

Best Local Similarity 100.0%; Score 45; DB 7; Length 9;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IMDOVPPSV 9

Db 1 IMDOVPPSV 9

Search completed: December 8, 2004, 17:16:41  
Job time : 11.2927 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 8, 2004, 17:06:18; Search time 1.7561 Seconds  
(without alignments)  
493.111 Million cell updates/sec

Title: US-10-073-301A-2

Perfect score: 45

Sequence: 1 IMPQVPRSV 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR.79.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	40	88.9	274	2	T16581	hypothetical prote
2	39	86.7	491	2	A49179	melanoma antigen h
3	39	86.7	626	2	S53871	Pmel 17 protein -
4	39	86.7	662	2	I38400	melanoma-associated
5	39	86.7	668	2	A41234	melanocyte-specific
6	33	73.3	350	2	T18848	LMK-2c - rat
7	33	73.3	439	2	E81291	hypothetical prote
8	33	73.3	617	1	I78847	LIM motif-containing
9	33	73.3	617	2	JC5814	LIM motif-containing
10	33	73.3	638	1	I78846	LIM motif-containing
11	33	73.3	638	2	JC5813	LIM motif-containing
12	32	71.1	128	2	E6178	probable transcrip
13	32	71.1	197	2	S65051	low molecular weigh
14	32	71.1	197	2	S72398	low molecular weigh
15	32	71.1	249	2	C90433	ABC transporter, A
16	32	71.1	258	2	T51689	probable transcrip
17	32	71.1	288	2	JC5262	leucine zipper pro
18	32	71.1	365	2	D86470	F21H2.9 protein -
19	32	71.1	633	2	E97999	hypothetical prote
20	32	71.1	633	2	H95128	ABC transporter, A
21	32	71.1	791	2	A53691	disacylglycerol kin
22	31	68.9	126	2	T32189	hypothetical prote
23	31	68.9	199	2	F71462	hypothetical prote
24	31	68.9	258	2	B97187	polysaccharide ABC
25	31	68.9	363	2	T19032	hypothetical prote
26	31	68.9	381	2	T13666	MDH2 dehydrogenas
27	31	68.9	609	2	T48762	probable ATP-depen
28	31	68.9	664	2	T35122	anthranilate synth
29	31	68.9	770	2	S00643	

30	31	68.9	770	2	S1161	anthranilate synth
31	31	68.9	837	2	I57557	DNA-binding protei
32	31	68.9	848	2	A54740	interleukin-4-indu
33	30	66.7	126	2	S77183	hypothetical prote
34	30	66.7	156	2	I49446	8-oxo-dGTPase - mo
35	30	66.7	200	2	E81314	probable periplasm
36	30	66.7	248	2	B83134	probable pili assem
37	30	66.7	263	2	E75046	hypothetical prote
38	30	66.7	319	2	D97205	hypothetical prote
39	30	66.7	388	2	D75353	yellow-related pro
40	30	66.7	389	2	H90413	conserved hypothet
41	30	66.7	390	2	A10396	multidrug resistanc
42	30	66.7	410	2	T38815	sepin homolog spn
43	30	66.7	455	2	T32189	zinc finger protei
44	30	66.7	474	2	T29336	hypothetical prote
45	30	66.7	482	2	T43996	vitron protein lim

#### ALIGNMENTS

```
RESULT 1
T16581
hypothetical protein K08A8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16581
R:Pauley, A.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid K08A8.
A:Reference number: Z18541
A:Accession: T16581
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-274 <PAU>
A:Cross-references: UNIPROT:Q21305; EMBL:U38377; NID:G1022968; PID:G1022970; PIDN:AAA79
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:K08A8.2
A:Introns: 50/2; 71/3; 113/3; 148/3

Query Match      88.9%; Score 40; DB 2; Length 274;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 IMPQVPRSV 9
DB      176 VMDQIPFSL 184

RESULT 2
A49179
melanoma antigen homolog rpel - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A49179; I45861
R:Kim, R.Y.; Wistow, G.U.
Exp. Eye Res. 55, 657-662, 1992
A:Title: The CDNA RPE1 and monoclonal antibody HMB-50 define gene products preferential
A:Reference number: A49179; MUID:53122163; PMID:1478275
A:Accession: A49179
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-491 <KIM>
A:Cross-references: UNIPROT:Q06154
A:Experimental source: retinal pigment epithelium
A:Note: sequence extracted from NCBI backbone (NCBIN:122438, NCBIIP:122439)
C:Genetics:
A:Gene: RPE1

Query Match      86.7%; Score 39; DB 2; Length 491;
Best Local Similarity 88.9%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 IMDOVPSV 9  
| | | | |  
Db 52 ITDOVPSV 60

## RESULT 3

S53871  
Pmel 17 protein - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C/Accession: S53871  
R/Kwon, B.S.; Halaban, R.; Ponnazhagan, S.; Kim, K.; Chintamaneni, C.; Bennett, D.; Pick  
Nucleic Acids Res. 23, 154-158, 1995  
A/Title: Mouse silver mutation is caused by a single base insertion in the putative cyto  
A/Reference number: S53871; MUID:95175358; PMID:7870580  
A/Accession: S53871  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-626 <KMO>  
A/Cross-references: UNIPROT:Q60696; GB:U14133; NID:g887940; PIDN:AAA69538.1; PID:g887941

Query Match 86.7%; Score 39; DB 2; Length 626;  
Best Local Similarity 88.9%; Pred. No. 4.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IMDOVPSV 9  
| | | | |  
Db 209 ITDOVPSV 217

## RESULT 4

I38400  
melanoma-associated ME20 antigen (me20m) - human  
N/Alternate names: melanoma antigen 25  
C/Species: Homo sapiens (man)  
C/Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
C/Accession: I38400; A53668; A55753  
R/Mareeh, G.A.; Marken, J.S.; Neubauer, M.; Aruffo, A.; Hellstrom, I.; Hellstrom, K.; Ma  
DNA Cell Biol. 13, 87-95, 1994  
A/Title: Cloning and expression of the gene for the Melanoma-Associated ME20 Antigen.  
A/Reference number: I38400; MUID:94235165; PMID:8179825  
A/Accession: I38400  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-662 <RES>  
A/Cross-references: UNIPROT:P40967; EMBL:U01874; NID:g494939; PIDN:AA18479.1; PID:g4949  
R/Adema, G.J.; de Boer, A.J.; Vogel, A.M.; Ionen, W.A.M.; Figdor, C.G.  
J. Biol. Chem. 269, 20126-20133, 1994  
A/Title: Molecular characterization of the melanocyte lineage-specific antigen gp100.  
A/Reference number: A53668; MUID:94327568; PMID:7519602  
A/Accession: A53668  
A/Molecule type: mRNA  
A/Residues: 1-592,594-662 <ADE>  
A/Cross-references: GB:73003; NID:g639589; PIDN:AA60634.1; PID:g639590  
R/Kawakami, Y.; Elyhu, S.; Delgado, C.H.; Robbins, P.F.; Sakaguchi, K.; Appella, E.; Y  
Proc. Natl. Acad. Sci. U.S.A. 91, 6458-6462, 1994  
A/Title: Identification of a human melanoma antigen recognized by tumor-infiltrating lym  
A/Accession: A55753  
A/Status: nucleic acid sequence not shown; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-161,163-592,594-662 <KAM>  
C/Keywords: glycoprotein

## Query Match

86.7%; Score 39; DB 2; Length 662;  
Best Local Similarity 88.9%; Pred. No. 4.9;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IMDOVPSV 9  
| | | | |  
Db 209 ITDOVPSV 217

RESULT 5  
A41234  
melanocyte-specific protein Pmel-17 precursor - human

C/Species: Homo sapiens (man)  
C/Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 30-Sep-1993  
C/Accession: A41234  
R/Kwon, B.S.; Chintamaneni, C.; Kozak, C.A.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.  
Proc. Natl. Acad. Sci. U.S.A. 88, 9228-9232, 1991  
A/Title: A melanocyte-specific gene, Pmel 17, maps near the silver coat color locus on "  
A/Reference number: A41234; MUID:92021023; PMID:1924386  
A/Accession: A41234  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-668 <KMO>  
A/Cross-references: GB:W77348

Query Match 86.7%; Score 39; DB 2; Length 668;  
Best Local Similarity 88.9%; Pred. No. 4.9;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IMDOVPSV 9  
| | | | |  
Db 209 ITDOVPSV 217

## RESULT 6

I78848  
LIMK-2c - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C/Accession: I78848  
R/Nunoue, K.; Chashit, K.; Okano, I.; Mizuno, K.  
Oncogene 11, 701-710, 1995  
A/Title: LIMK-1 and LIMK-2, two members of a LIM motif-containing protein kinase family  
A/Reference number: I58353; MUID:95380177; PMID:7651734  
A/Accession: I78848  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-350 <RES>  
A/Cross-references: UNIPROT:P53670; GB:D31876; NID:g1684614; PIDN:BA06675.1; PID:g1000  
F/51-103/Domain: LIM metal-binding repeat homology <LIM2>

Query Match 73.3%; Score 33; DB 2; Length 350;  
Best Local Similarity 55.6%; Pred. No. 4.4;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 IMDOVPSV 9  
| | | | |  
Db 121 VDOQLPSV 129

## RESULT 7

E81291  
hypothetical protein Cj1454c [imported] - Campylobacter jejuni (strain NCTC 1168)  
C/Species: Campylobacter jejuni  
C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C/Accession: E81291  
R/Parikh, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Church, C.; Basham, D.; Chilli,  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre  
Nature 403, 665-668, 2000  
A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy  
A/Reference number: A81250; MUID:20150912; PMID:10688204  
A/Accession: E81291  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-439 <DAR>  
A/Cross-references: UNIPROT:Q9PMK6; GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CA8738  
A/Experimental source: serotype O2, strain NCTC 11168  
C/Genetics:  
A/Gene: Cj1454c  
C/Superfamily: conserved hypothetical protein b0835

Query Match 73.3%; Score 33; DB 2; Length 439;  
 Best Local Similarity 75.0%; Pred. No. 56;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 MDQVPSV 9  
 Db 335 MDQVPSV 342

## RESULT 8

178847 LIM motif-containing protein kinase (BC 2.7.1.-) 2, splice form b [similarity] - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 09-Jul-2004  
 C/Accession: 178847; 178849  
 R/Nunoue, K.; Ohashi, K.; Mizuno, K.  
 Oncogene 11, 701-710, 1995  
 A/Title: LIMK-1 and LIMK-2, two members of a LIM motif-containing protein kinase family  
 A/Reference number: 158353; MUID:95380177; PMID:7651734  
 A/Accession: 178847  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-617 <RES>  
 A/Cross-references: UNIPROT:P53670; GB:D31875; NID:g1684613; PDB:BAA06674.1; PID:g10006  
 A/Accession: 178849  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-163 <RES2>  
 A/Cross-references: GB:D31877; NID:g1684615; PDB:BAA06676.1; PID:g1000690  
 C/Genetic: <RES1>  
 A/Gene: Link-2b  
 C/Genetic: <RES2>  
 A/Gene: Link-2d  
 C/Superfamily: LIM protein kinase; LIM metal-binding repeat homology; protein kinase hom  
 C/Keywords: alternative splicing; ATP; duplication; phosphotransferase; serine/threonine  
 F/51-103/Domain: LIM metal-binding repeat homology <LIM2>  
 F/308-587/Domain: protein kinase homology <KIN>  
 F/316-324/Region: protein kinase ATP-binding motif

Query Match 73.3%; Score 33; DB 1; Length 617;  
 Best Local Similarity 55.6%; Pred. No. 82;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 IMDQVPSV 9  
 Db 121 VQDQLPSV 129

## RESULT 9

JC5814 LIM motif-containing protein kinase (BC 2.7.1.-) 2, splice form b - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 09-Jul-2004  
 C/Accession: JC5814  
 R/Koshimizu, U.; Takahashi, H.; Yoshida, M.C.; Nakamura, T.  
 Biochem. Biophys. Res. Commun. 241, 243-250, 1997  
 A/Title: cDNA cloning, genomic organization, and chromosomal localization of the mouse I  
 A/Reference number: JC5813; MUID:98086337; PMID:9425257  
 A/Accession: JC5814  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-617 <KOS>  
 A/Cross-references: UNIPROT:O54785; DDBJ:AB008119  
 A/Experimental source: embryo  
 C/Comment: This enzyme is involved in a signal transduction pathway to regulate various  
 C/Genetic:  
 A/Gene: Link2b  
 A/Map position: 1d  
 C/Superfamily: LIM protein kinase; LIM metal-binding repeat homology; protein kinase hom  
 C/Keywords: alternative splicing; phosphotransferase  
 F/51-103/Domain: LIM metal-binding repeat homology <LIM2>  
 F/308-587/Domain: protein kinase homology <KIN>  
 F/317-580/Domain: protein kinase #status predicted <PKD>

Query Match 73.3%; Score 33; DB 2; Length 617;  
 Best Local Similarity 55.6%; Pred. No. 82;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 IMDQVPSV 9  
 Db 121 VQDQLPSV 129

## RESULT 10

178846 LIM motif-containing protein kinase (BC 2.7.1.-) 2, splice form a [similarity] - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 09-Jul-2004  
 C/Accession: 178846  
 R/Nunoue, K.; Ohashi, K.; Mizuno, K.  
 Oncogene 11, 701-710, 1995  
 A/Title: LIMK-1 and LIMK-2, two members of a LIM motif-containing protein kinase family  
 A/Reference number: 158353; MUID:95380177; PMID:7651734  
 A/Accession: 178846  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-638 <RES>  
 A/Cross-references: UNIPROT:P53670; GB:D31874; NID:g1684612; PDB:BAA06673.1; PID:g1000  
 A/Experimental source: strain Wistar; tissue brain  
 C/Genetic:  
 A/Gene: Link-2a  
 C/Superfamily: LIM protein kinase; LIM metal-binding repeat homology; protein kinase ho  
 C/Keywords: alternative splicing; ATP; duplication; phosphotransferase; serine/threonin  
 F/12-63/Domain: LIM metal-binding repeat homology <LIM1>  
 F/72-124/Domain: LIM metal-binding repeat homology <LIM2>  
 F/329-608/Domain: protein kinase homology <KIN>  
 F/337-345/Region: protein kinase ATP-binding motif

Query Match 73.3%; Score 33; DB 1; Length 638;  
 Best Local Similarity 55.6%; Pred. No. 85;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 IMDQVPSV 9  
 Db 142 VQDQLPSV 150

## RESULT 11

JC5813 LIM motif-containing protein kinase (BC 2.7.1.-) 2, splice form a - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 09-Jul-2004  
 C/Accession: JC5813  
 R/Koshimizu, U.; Takahashi, H.; Yoshida, M.C.; Nakamura, T.  
 Biochem. Biophys. Res. Commun. 241, 243-250, 1997  
 A/Title: cDNA cloning, genomic organization, and chromosomal localization of the mouse  
 A/Reference number: JC5813; MUID:98086337; PMID:9425257  
 A/Accession: JC5813  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-638 <KOS>  
 A/Cross-references: UNIPROT:O54785; DDBJ:AB008117; NID:g2789463; PID:g2789464  
 A/Experimental source: embryo  
 C/Comment: This enzyme is involved in a signal transduction pathway to regulate various  
 C/Genetic:  
 A/Gene: Link2a  
 A/Map position: 1d  
 C/Superfamily: LIM protein kinase; LIM metal-binding repeat homology; protein kinase ho  
 C/Keywords: alternative splicing; phosphotransferase  
 F/12-63/Domain: LIM metal-binding repeat homology <LIM1>  
 F/72-124/Domain: LIM metal-binding repeat homology <LIM2>  
 F/329-608/Domain: protein kinase homology <KIN>  
 F/338-601/Domain: protein kinase #status predicted <PKD>

Query Match 73.3%; Score 33; DB 2; Length 638;  
 Best Local Similarity 55.6%; Pred. No. 85;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 IMOVPPSV 9  
 : ||: ||  
 Db 142 VQDQIPRVS 150

RESULT 12  
 E46178  
 probable transcription factor fork head domain 5 (FDS) - fruit fly (*Drosophila melanogaster*)  
 C/Species: *Drosophila melanogaster*  
 C/Date: 22-Sep-1993 #sequence\_revision 25-Apr-1997 #text\_change 16-Aug-2004  
 C/Accession: E46178  
 R/Lafayette, U.; Grossniklaus, U.; Gehring, M.J.; Jackle, H.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 8754-8758, 1992  
 A/Title: Developmentally regulated *Drosophila* gene family encoding the fork head domain.  
 A/Reference number: A46178; MUID:92409595; PMID:11356269  
 A/Accession: E46178  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: nucleic acid  
 A/Residues: 1-128 <HAC>  
 A/Cross-references: UNIPROT:P32029; GB:M66444; NID:g157431; PIDN:AAF02178.1; PID:g604218  
 A/Note: sequence extracted from NCBI backbone (NCBI:P114227)  
 C/Superfamily: fork head DNA-binding domain homology  
 F/16-107/Domain: fork head DNA-binding domain homology <FHD>

Query Match 71.1%; Score 32; DB 2; Length 128;  
 Best Local Similarity 85.7%; Pred. No. 24;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IMOVPPSV 7  
 : ||| ||  
 Db 46 IMOVPPSV 52

RESULT 13  
 S65051  
 low molecular weight heat shock protein precursor (clone Hsp22.5), endoplasmic reticulum  
 C/Species: Glycine max (soybean)  
 C/Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S65051  
 R/Lafayette, P.R.; Nagao, R.T.; O'Grady, K.; Vierling, E.; Key, J.L.  
 Plant Mol. Biol. 30, 159-169, 1996  
 A/Title: Molecular characterization of cDNAs encoding low-molecular-weight heat shock pr  
 A/Reference number: S65049; MUID:96197406; PMID:8616233  
 A/Accession: S65051  
 A/Status: preliminary; nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-197 <LAF>  
 A/Cross-references: UNIPROT:Q39820; EMBL:U21724  
 C/Keywords: heat shock

Query Match 71.1%; Score 32; DB 2; Length 197;  
 Best Local Similarity 44.4%; Pred. No. 38;  
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 IMOVPPSV 9  
 : ||: ||  
 Db 51 VLEQIPRVS 59

RESULT 14  
 S72398  
 low molecular weight heat shock protein precursor (clone Hsp22.5), endoplasmic reticulum  
 C/Species: Glycine max (soybean)  
 C/Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S72398  
 R/Lafayette, P.R.  
 submitted to the EMBL Data Library, February 1995  
 A/Reference number: S72398  
 A/Accession: S72398  
 A/Status: preliminary  
 A/Molecule type: mRNA

A/Residues: 1-197 <LAF>  
 A/Cross-references: UNIPROT:Q39820; EMBL:U21724; NID:g710435; PIDN:AAE03098.1; PID:g710435

Query Match 71.1%; Score 32; DB 2; Length 197;  
 Best Local Similarity 44.4%; Pred. No. 38;  
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 IMOVPPSV 9  
 : ||: ||  
 Db 51 VLEQIPRVS 59

RESULT 15  
 C90433  
 ABC transporter, ATP binding protein SSO2600 [imported] - *Sulfolobus solfataricus*  
 C/Species: *Sulfolobus solfataricus*  
 C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 16-Aug-2004  
 C/Accession: C90433  
 R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyaz, M.J.; Chan-  
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, J.  
 arrest. R.A.; Ragan, M.A.; Sersen, C.W.; Van der Oost, J.  
 submitted to GenBank, April 2001  
 A/Description: *Sulfolobus solfataricus* complete genome.  
 A/Reference number: A99139  
 A/Accession: C90433  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-249 <KUR>  
 A/Cross-references: UNIPROT:Q97VM2; GB:AE006641; NID:g13815904; PIDN:AAK42722.1; GSPDB:  
 C/Genetics:  
 A/Gene: SSO2600  
 C/Superfamily: ATP-binding cassette homology

Query Match 71.1%; Score 32; DB 2; Length 249;  
 Best Local Similarity 85.7%; Pred. No. 49;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IMOVPPSV 7  
 : ||| ||  
 Db 54 IMOVPPSV 60

Search completed: December 8, 2004, 17:13:37  
 Job time : 5.7561 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 8, 2004, 17:06:18 ; Search time 6.91463 Seconds

(without alignments)  
748.900 Million cell updates/sec

Title: US-10-073-301A-2

Perfect score: 45

Sequence: 1 IMDOVPPSV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	88.9	199	2	Q8IG08
2	40	88.9	283	2	Q21305
3	39	86.7	461	2	Q97884
4	39	86.7	491	1	PM17_BOVIN
5	39	86.7	626	1	PM17_MOUSE
6	39	86.7	626	2	Q9CZB2
7	39	86.7	661	1	PM17_HUMAN
8	39	86.7	661	2	AAH35866
9	37	82.2	684	2	Q7ZVU9
10	36	80.0	664	2	Q7ZBS2
11	36	80.0	964	2	AAH59640
12	35	77.8	316	2	Q7XUY6
13	35	77.8	417	2	Q9F6E7
14	35	77.8	638	2	Q7MJG0
15	34	75.6	149	2	Q94CH0
16	34	75.6	342	2	Q6PBN3
17	34	75.6	342	2	AAH59645
18	34	75.6	345	1	RDS1_XENLA
19	34	75.6	345	2	Q7SYF6
20	34	75.6	402	2	Q7MDZ6
21	34	75.6	402	2	Q8D607
22	34	75.6	3167	2	Q7QO87
23	33	73.3	98	2	Q9OMM3
24	33	73.3	239	2	Q9ZOM1
25	33	73.3	315	2	Q8IRR3
26	33	73.3	337	2	Q7LYI2
27	33	73.3	337	2	Q9HH23
28	33	73.3	337	2	Q9HH28
29	33	73.3	390	2	Q82DI8
30	33	73.3	422	2	Q6NX08
31	33	73.3	422	2	Q803T7

32	33	73.3	422	2	AAH67331	Aah67331 brachydan
33	33	73.3	439	2	Q9PMK6	Q9pmk6 campylobact
34	33	73.3	556	2	Q98K51	Q98k51 rhizobium l
35	33	73.3	614	2	Q7UT24	Q7ut24 rhizobium l
36	33	73.3	617	2	AAH65578	Aah65578 rattus no
37	33	73.3	638	1	LIK2_MOUSE	lik2 mus musculus
38	33	73.3	638	1	LIK2_RAT	lik2 rattus norv
39	33	73.3	668	2	Q86ZT6	Q86zt6 alternaria
40	33	73.3	1145	2	Q7Z8T3	Q7z8t3 cochlidiobol
41	33	73.3	1239	2	Q6SLC7	Q6slc7 cochlidiobol
42	33	73.3	1239	2	AAH29899	Aah29899 cochlidiob
43	33	73.3	1329	2	Q7Z8T6	Q7z8t6 cochlidiobol
44	33	73.3	1329	2	Q7Z8T7	Q7z8t7 cochlidiobol
45	33	73.3	1329	2	Q7Z8T8	Q7z8t8 cochlidiobol

## ALIGNMENTS

## RESULT 1

ID	Q8IG08	PRELIMINARY;	PRT;	199 AA.
AC	Q8IG08;			
DT	01-MAR-2003 (TREMURel. 23, Created)			
DT	01-MAR-2003 (TREMURel. 23, last sequence update)			
DT	01-MAR-2004 (TREMURel. 26, last annotation update)			
DE	Sox (Mammalian soy box) family protein 2, isoform b.			
GN	Name=sox-2; ORFNames=K08A8.2;			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabdilitidae;			
CC	Rhabdilitidae; Peloderinae; Caenorhabditis.			
OK	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RX	MEDLINE=99069613; PubMed=9851916;			
RA	Wilson R.;			
RT	"Genome sequence of the nematode C. elegans: a platform for			
RT	investigating biology. The C. elegans Sequencing Consortium.;"			
RL	Science 282:2012-2018 (1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.			
RL	Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; U38377; AAN72421.1; -.			
DR	HSSP; P48432; 1GTO.			
DR	WormPep; K08A8.2b; CE31200.			
DR	GO:0003677; F:DNA binding; IEA.			
DR	GO:0006355; P:regulation of transcription, DNA-dependent; IEA.			
DR	InterPro; IPR009071; HMG-box.			
DR	InterPro; IPR00910; HMG_12_box.			
DR	Pfam; PF00505; HMG_box; 1.			
DR	SMART; SM00398; HMG; 1.			
DR	PROSITE; PS0118; HMG_BOX_2; 1.			
SO	SEQUENCE 199 AA; 22734 MW; D737C6B75EDB944 CRC64;			
QY	Query Match	88.9%;	Score 40;	DB 2; Length 199;
	Best Local Similarity	66.7%;	Pred. No. 2.5;	
	Matches	6; Conservative	3; Mismatches	0; Indels
				Gaps 0;



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FT DOMAIN 445 491 Cytoplasmic (Potential).
FT DOMAIN 60 150 PKD.
FT DOMAIN 148 256 8 X 13 AA approximate tandem repeats.
FT REPEAT 148 256 1.
FT REPEAT 161 173 2.
FT REPEAT 174 186 3.
FT REPEAT 187 199 4.
FT REPEAT 200 212 5.
FT REPEAT 213 225 6.
FT REPEAT 232 243 7.
FT REPEAT 244 256 8.
FT DOMAIN 304 394 Cys-rich.
FT CARBOHYD 269 269 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 396 396 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 491 AA; 51669 MW; 288F5EDFD397D6D CRC64;

Query Match 86.7%; Score 39; DB 1; Length 491;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IMDOVPSV 9
Db 52 ITDOVPSV 60

RESULT 5
PM17 MOUSE STANDARD; PRT; 626 AA.
AC Q60696;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Melanocyte protein Pmel 17 precursor (Silver locus protein).
GN Name=Silv; Synonyms=Pmel17, D10H1253E, Sl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND VARIANTS SILVER.
RC STRAIN=C57BL/6; Tissue=Skin;
RX MEDLINE=95175358; PubMed=7870580;
RA Kwon B.S., Halaban R., Ponnazhagan S., Kim K., Chintamani C.,
RA Bennett D., Pickard R.T.;
RT "Mouse silver mutation is caused by a single base insertion in the
RT putative cytoplasmic domain of Pmel 17.";
RL Nucleic Acids Res. 23:154-158(1995).
CC -1- FUNCTION: Could be a melanogenic enzyme.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Preferentially expressed in melanocytes.
CC -1- DISEASE: Defects in Silv are the cause of the silver coat color
CC which seems to be due to premature death of pigment cells during
CC the hair cycle.
CC -1- SIMILARITY: Belongs to the Pmel-17/MBF family.
CC -1- SIMILARITY: Contains 1 PKD domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; U14133; AAA69538.1; -.
DR PIR; S53871; S53871.
DR MGD; MGI:98301; Sl.
DR InterPro; IPR000601; PKD.
DR Pfam; PF00801; PKD; 1.
DR PROSITE; PS50093; PKD; 1.
KW Disease mutation; Glycoprotein; Melanin biosynthesis; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 24 Potential.

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FT CHAIN 25 626 Melanocyte protein Pmel 17.
FT DOMAIN 25 562 Extracellular (Potential).
FT TRANSMEM 563 583 Potential.
FT DOMAIN 584 626 Cytoplasmic (Potential).
FT DOMAIN 315 411 PKD.
FT REPEAT 315 327 1.
FT REPEAT 328 340 2.
FT REPEAT 341 353 3.
FT REPEAT 354 366 4.
FT REPEAT 367 379 5.
FT REPEAT 380 392 6.
FT REPEAT 393 411 7.
FT CARBOHYD 81 81 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 106 106 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 111 111 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 535 535 N-linked (GlcNAc...) (Potential).
FT VARIANT 170 170 S -> L (in silver).
FT VARIANT 175 175 R -> G (in silver).
FT VARIANT 373 373 D -> N (in silver).
FT VARIANT 471 471 F -> S (in silver).
FT VARIANT 603 626 AAPASGIRARGLGNSPLSGQGV -> SSASLRSSRPBW
RKQAPQWTGRIIRKAPWISWG (in silver).

SQ SEQUENCE 626 AA; 65980 MW; 7AB941D2E3FB1044 CRC64;

Query Match 86.7%; Score 39; DB 1; Length 626;
Best Local Similarity 88.9%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IMDOVPSV 9
Db 209 ITDOVPSV 217

RESULT 6
Q9CZB2 PRELIMINARY; PRT; 626 AA.
ID Q9CZB2;
AC Q9CZB2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2810025C24 product:silver, full insert
DE sequence.
GN Name=Sl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Whole body;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Whole body;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Whole body;
RA The PANTOM Consortium;
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.

```

RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=2049374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama J., Nishi K., Kizunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsubara S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.",  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,  
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
 RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,  
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,  
 RA Okazaki Y., Okido T., Owa C., Saito R., Saito R., Sakai C., Sakai K.,  
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,  
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.,  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AK012808; BAB28486.1; -.  
 DR MGD; MGI:98301; Sl.  
 DR InterPro; IPR00601; PKD.  
 DR Pfam; PF00801; PKD.1.  
 DR SMART; SM00089; PKD.1.  
 DR PROSITE; PSS0093; PKD.1.  
 SQ SEQUENCE 626 AA; 66301 MW; 7EC0A06C63212674 CRC64;  
 Query Match 86.7%; Score 39; DB 2; Length 626;  
 Best Local Similarity 88.9%; Pred. NO. 14;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 IMPDQPSV 9  
 Db 208 ITDQVPSV 216  
 RESULT 7  
 ID PM17 HUMAN STANDARD; PRT; 661 AA.  
 AC P40967; Q12763; Q14448; Q14817; Q16565;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Melanocyte protein Pmel 17 precursor (Melanocyte lineage-specific  
 DE antigen GP100) (Melanoma-associated ME20 antigen) (ME20W/ME20S) (ME20-  
 DE M/ME20-S) (95 kDa melanocyte-specific secreted glycoprotein).  
 GN Name-Slly; Synonyms=PMEL17, D12S53E;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92021023; PubMed=1924386;  
 RA Kwon B.S., Chintamaneni C., Kozak C.A., Copeland N.G., Gilbert D.J.,  
 RA Jenkins N.A., Barton D., Francke U., Kobayashi Y., Kim K.-K.;

RT "A melanocyte-specific gene, Pmel 17, maps near the silver coat color  
 RT locus on mouse chromosome 10 and is in a syntenic region on human  
 RT chromosome 12.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9228-9232(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9437568; PubMed=7519602;  
 RA Adema G.J., de Boer A.J., Vogel A.M., Loenen W.A., Figdor C.G.,  
 RT "Molecular characterization of the melanocyte lineage-specific antigen  
 RT gp100.";  
 RL J. Biol. Chem. 269:20126-20133(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96154052; PubMed=8592076;  
 RA Bailly T., Lee S.-T., Spritz R.A.,  
 RT "Genomic organization and sequence of D12S53E (Pmel 17), the human  
 RT homologue of the mouse silver (S1) locus.";  
 RL J. Invest. Dermatol. 106:24-27(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-53.  
 RX MEDLINE=94235165; PubMed=8179825;  
 RA Mareeh G.A., Marken J.S., Neubauer M., Aruffo A., Hellstrom I.,  
 RA Hellstrom K.E., Margardt H.,  
 RT "Cloning and expression of the gene for the melanoma-associated ME20  
 RT antigen.";  
 RL DNA Cell Biol. 13:87-95(1994).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96314705; PubMed=8739560;  
 RA Kim K.-K., Youn B.S., Heng H.H., Shi X.-M., Tsui L.-C., Lee Z.H.,  
 RA Pickard R.T., Kwon B.S.,  
 RT "Genomic organization and FISH mapping of human Pmel 17, the putative  
 RT silver locus.";  
 RL Pigment Cell Res. 9:42-48(1996).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Vogel A.,  
 RT Submitted (NOV-1990) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins L., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -I- FUNCTION: Could be a melanogenic enzyme. Could represent an  
 CC oncofetal self-antigen that is normally expressed at low levels in  
 CC quiescent adult melanocytes but overexpressed by proliferating  
 CC neonatal melanocytes and during tumor growth. Release of the  
 CC soluble form, ME20-S, could protect tumor cells from antibody  
 CC mediated immunity.  
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (Potential). There  
 CC is also a secreted soluble form, ME20-S, probably product of  
 CC proteolytic cleavage.  
 CC TISSUE SPECIFICITY: Preferentially expressed in melanomas. Some  
 CC expression was found in dysplastic nevi. Not found in normal



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CC      license nor in Carcinomas. Pmel-17/NMB family.
CC      -1- SIMILARITY: Belongs to the Pmel-17/NMB family.
CC      -1- SIMILARITY: Contains 1 PKD domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M77348; AAA60121.1; -
DR      EMBL; S73003; AAC60534.1; -
DR      EMBL; U31799; AAB00386.1; -
DR      EMBL; U31808; AAB00386.1; JOINED.
DR      EMBL; U31807; AAB00386.1; JOINED.
DR      EMBL; U31797; AAB00386.1; JOINED.
DR      EMBL; U31798; AAB00386.1; JOINED.
DR      EMBL; U01874; AAB18479.1; -
DR      EMBL; U20093; AAB19181.1; -
DR      EMBL; U19491; AAB19181.1; JOINED.
DR      EMBL; M32295; AAA35930.1; ALT_INTR.
DR      EMBL; BC001414; AAH01414.1; -
DR      PIR; I38400; I38400.
DR      Genew; HGNC:10880; SILV.
DR      MIM; 155550; -
DR      GO; GO:0005886; C:plasma membrane; TAS.
DR      InterPro; IPR00601; PKD.
DR      Pfam; PF00801; PKD; 1.
DR      PROSITE; PS50093; PKD; 1.
KW      Antigen; Direct protein sequencing; Glycoprotein;
KW      Melanin biosynthesis; Repeat; Signal; Transmembrane.
FT      CHAIN 1 24
FT      SIGNAL 1 24
FT      DOMAIN 25 661 Melanocyte protein Pmel 17.
FT      TRANSMM 596 616 Extracellular (Potential).
FT      DOMAIN 617 661 Potential.
FT      DOMAIN 255 292 Cytoplasmic (Potential).
FT      DOMAIN 315 444 10 X 13 AA approximate tandem repeats.
FT      REPEAT 327 327 1.
FT      REPEAT 328 340 2.
FT      REPEAT 341 353 3.
FT      REPEAT 354 366 4.
FT      REPEAT 367 379 5.
FT      REPEAT 380 392 6.
FT      REPEAT 393 405 7.
FT      REPEAT 406 418 8.
FT      REPEAT 419 431 9.
FT      REPEAT 432 444 10.
FT      CARBOHYD 81 106 N-linked (GlcNAc...) (Potential).
FT      CARBOHYD 106 106 N-linked (GlcNAc...) (Potential).
FT      CARBOHYD 111 111 N-linked (GlcNAc...) (Potential).
FT      CARBOHYD 121 321 N-linked (GlcNAc...) (Potential).
FT      CARBOHYD 568 568 N-linked (GlcNAc...) (Potential).
FT      CONFLICT 274 274 L -> P (in Ref. 1 and 5).
FT      CONFLICT 587 587 P -> PVEGILT (in Ref. 1).
FT      CONFLICT 592 592 G -> GG (in Ref. 4).
FT      CONFLICT 597 597 P -> R (in Ref. 1).
FT      CONFLICT 642 661 RIFCSPIGENSPILSGOV -> ASSALVPLVRIAPSSVG
SQ      SEQUENCE 661 AA; 70255 MW; 8A904FAB16715653 CRC64;
Query Match 86.7%; Score 39; DB 1; Length 661;
Best Local Similarity 88.9%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 IMDVPSV 9
Db 209 ITDVPFSV 217

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AAP35866
ID AAP35866 PRELIMINARY; PRT; 661 AA.
AC AAP35866;
DT 02-MAR-2004 (TRENBLREL 27, Created)
DT 02-MAR-2004 (TRENBLREL 27, Last sequence update)
DT 02-MAR-2004 (TRENBLREL 27, Last annotation update)
DE Silver homolog (Mouse).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kairine N., Chen X., Rolfe A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael A., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
RT vector";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT007202; AAP35866.1; -
SQ SEQUENCE 661 AA; 70255 MW; 8A904FAB16715653 CRC64;
Query Match 86.7%; Score 39; DB 2; Length 661;
Best Local Similarity 88.9%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 IMDVPSV 9
Db 209 ITDVPFSV 217

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RESULT 9
OZVU9 PRELIMINARY; PRT; 684 AA.
ID OZVU9;
AC OZVU9;
DT 01-JUN-2003 (TRENBLREL 24, Created)
DT 01-JUN-2003 (TRENBLREL 24, Last sequence update)
DT 01-MAR-2004 (TRENBLREL 26, Last annotation update)
DE Nup1 protein (Fragment).
GN Name=nup1;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skelton U., Smallie D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE FROM N.A.
RP STRAIN=AB; TISSUE=Whole body;
RA Strauberg R.;

```

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC045402; AAH45402.1; -.  
DR ZFIN: ZDB-GENE-030131-9837; nmpl.  
DR InterPro: IPR010301; Nop52.  
DR Pfam: PF05997; Nop52; 1.  
DR NCN TER 1  
SQ SEQUENCE 684 AA; 77380 MW; DC5014B08FECBCC6 CRC64;

Query Match 82.2%; Score 37; DB 2; Length 684;  
Best Local Similarity 66.7%; Pred. No. 44;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IMDOVPSV 9  
|:|||||:  
Db 232 IVDQVPFAI 240

RESULT 10  
Q72BS2 PRELIMINARY; PRT; 964 AA.  
ID Q72BS2  
AC Q72BS2;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE HAMP domain protein.  
GN OrderedLocustNames=DVU1562;  
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303).  
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;  
OC Desulfobacteriaceae; Desulfobacteriales;  
OC Desulfobacteriaceae; Desulfobacteriales;  
OC NCB1\_TaxID=882;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=15077118; DOI=10.1038/nbt959;  
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,  
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,  
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,  
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,  
RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Radune D.,  
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Uitterback T.R.,  
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;  
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium  
RT Desulfovibrio vulgaris Hildenborough.";  
RL Nat. Biotechnol. 22:554-559(2004).  
DR EMBL: AE017314; AAS96040.1; -.  
DR TIGR: DVU1562; -.  
DR InterPro: IPR003018; GAF.  
DR InterPro: IPR003660; HAMP.  
DR InterPro: IPR003607; Met\_phos\_hydro.  
DR Pfam: PF01590; GAF; 1.  
DR Pfam: PF00672; HAMP; 1.  
DR SMART: SM00471; HDC; 1.  
KM Complete proteome.  
SQ SEQUENCE 964 AA; 107427 MW; C3E9682BBE43CC79 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 964;  
Best Local Similarity 75.0%; Pred. No. 1,1e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IMDOVPSV 8  
|:|||||:  
Db 542 VIDQVPS 549

RESULT 11  
AAS96040 PRELIMINARY; PRT; 964 AA.  
ID AAS96040  
AC AAS96040;  
DT 27-APR-2004 (TrEMBLrel. 27, Created)  
DT 27-APR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 11-MAY-2004 (TrEMBLrel. 27, Last annotation update)  
DE HAMP domain protein.  
GN DVU1562.

OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303).  
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;  
OC Desulfobacteriaceae; Desulfobacteriales;  
OC NCB1\_TaxID=882;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=15077118;  
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,  
RA Kolonay J.F., Eisen J.A., Ward N., Methe B.A., Brinkac L.M.,  
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,  
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,  
RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Radune D.,  
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Uitterback T.R.,  
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;  
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium  
RT Desulfovibrio vulgaris Hildenborough.";  
RL Nat. Biotechnol. 22:554-559(2004).  
DR EMBL: AE017314; AAS96040.1; -.  
DR TIGR: DVU1562; -.  
SQ SEQUENCE 964 AA; 107427 MW; C3E9682BBE43CC79 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 964;  
Best Local Similarity 75.0%; Pred. No. 1,1e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IMDOVPSV 8  
|:|||||:  
Db 542 VIDQVPS 549

## RESULT 12

Q7XUY6 PRELIMINARY; PRT; 316 AA.

ID Q7XUY6  
AC Q7XUY6;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE OSUJNB0048E02.11 protein.  
GN Name=OSUJNB0048E02.11;  
OS Oryza sativa (japonica cultivar-group). Embryophyta; Tracheophyta;  
OC Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta; Poaceae;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Eriarthroideae; Oryzoideae; Oryzae; Oryza.  
OX NCB1\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=12447439;  
RA Pang Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,  
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,  
RA Wang Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,  
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,  
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,  
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,  
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,  
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,  
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,  
RA Han B.;  
RT "Sequence and analysis of rice chromosome 4.";  
RL Nature 420:316-320(2002).  
DR EMBL: AL606653; CAD40935.1; -.  
DR Gramene: Q7XUY6; -.  
DR GO: GO:0008080; F:N-acetyltransferase activity; IEA.  
DR InterPro: IPR000182; GCN5acetyl\_trans.  
DR Pfam: PF00583; Acetyltransferase\_1; 1.  
SQ SEQUENCE 316 AA; 34542 MW; 36C799C4C038EC66 CRC64;

Query Match 77.8%; Score 35; DB 2; Length 316;  
Best Local Similarity 66.7%; Pred. No. 53;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IMDOVPSV 9  
|:|||||:  
Db 542 VIDQVPS 549

Db 256 IIDVPRNM 264

## RESULT 13

ID Q9F6E7 PRELIMINARY; PRT; 417 AA.  
AC Q9F6E7;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE PKSA beta-ketoacylsynthase subunit beta.  
OS Streptomyces collinus.  
OC Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;  
OC Streptomyces; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=42684;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM2012;  
RL Martin R., Bailey J.E., Minas W.;  
CC Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF293354; AAC26880.1; -.  
DR HSSP; P73283; 1B5M.  
DR GO; GO:0016740; P:transferase activity; IEA.  
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.  
DR InterPro; IPR000794; K:ketocacyl\_synth.  
DR Pfam; PF00109; K:ketocacyl\_synth.1.  
DR Pfam; PF02801; K:ketocacyl\_synth\_C; 1.  
KM Transferase.  
SQ SEQUENCE 417 AA; 43370 MW; 483FAB4A31205AD CRC64;

Query Match 77.8%; Score 35; DB 2; Length 417;  
Best Local Similarity 66.7%; Pred. No. 71;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IMDOVPSV 9  
Db 98 VTDEVPFSV 106

## RESULT 14

ID Q7MJG0 PRELIMINARY; PRT; 638 AA.  
AC Q7MJG0;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Type I restriction-modification system methyltransferase subunit.  
GN Name=V2292;  
OS Vibrio vulnificus (strain VJ016).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrrio.  
OX NCBI\_TaxID=196600;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=1465965;  
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,  
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,  
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;  
RT "Comparative genome analysis of Vibrio vulnificus, a marine  
pathogen."  
RL Genome Res. 13:2577-2587(2003).  
DR EMBL; AP005338; BAC94966.1; -.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0008170; F:N-methyltransferase activity; IEA.  
DR GO; GO:0009007; F:site-specific DNA-methyltransferase (adenin. . .); IEA.  
DR GO; GO:0016740; P:transferase activity; IEA.  
DR GO; GO:0006306; P:DNA methylation; IEA.  
DR InterPro; IPR003665; M:DNA modification; IEA.  
DR InterPro; IPR002296; N12N6\_mtfase.  
DR InterPro; IPR003356; N6\_DNA\_mtfase.  
DR InterPro; IPR000055; RecT\_mod\_DNA.

DR Pfam; PF02506; Methylase\_M; 1.  
DR Pfam; PF01420; Methylase\_S; 1.  
DR Pfam; PF02384; N6\_Mcase; 1.  
DR PRINTS; PR00507; N12N6MTFRASE.  
KM Methyltransferase; Transferase.  
SQ SEQUENCE 638 AA; 71784 MW; 4D93E4496B30DF66 CRC64;

Query Match 77.8%; Score 35; DB 2; Length 638;  
Best Local Similarity 55.6%; Pred. No. 1,1e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IMDOVPSV 9  
Db 110 ILDOIPRRI 118

## RESULT 15

ID Q94CHO PRELIMINARY; PRT; 149 AA.  
AC Q94CHO;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Seven transmembrane protein M105 (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22456933; PubMed=12569425;  
RA Devoto A., Hartmann H.A., Piffaneli P., Elliott C., Simmons C.,  
RA Taramano G., Goh C.-S., Cohen P.E., Emerson B.C., Schultze-Lefert P.,  
RA Panstruga R.;  
RT "Molecular phylogeny and evolution of the plant-specific seven-  
transmembrane M10 family."  
RL J. Mol. Evol. 56:77-88(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Briggs S.P., Simmons C.R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY029316; AKX8341.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0008219; P:cell death; IEA.  
DR InterPro; IPR004326; M10.  
DR Pfam; PF03094; M10; 1.  
KM Transmembrane.  
FT NON\_TER 1  
SQ SEQUENCE 149 AA; 16260 MW; D037057B000EB9A4 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 149;  
Best Local Similarity 77.8%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IMDOVPSV 9  
Db 28 IMDHVPRIV 36

Search completed: December 8, 2004, 17:09:51.  
Job time : 13.9146 secs

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## OM protein - protein search, using sw model

Run on: December 8, 2004, 17:06:18 ; Search time 182.085 Seconds

(without alignments)  
748.900 Million cell updates/sec

Title: US-10-073-301a-9

Perfect score: 1272

Sequence: 1 QVXKQESGGGLVKGSGSLK.....TYQCEMSGVPYTRGGTKL 237

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: uniprot\_02.\*  
2: uniprot\_01.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	936.5	73.6	255	2	Q6KB05 mus musculu
2	936.5	73.6	255	2	Q6KB05 mus musculu
3	838	65.9	298	2	Q9QYF0 syntheic c
4	710.5	55.9	241	2	Q921A6 mus musculu
5	692.5	54.4	243	2	Q7TOM2 mus musculu
6	588	46.2	218	2	Q925S1 mus musculu
7	543.5	42.7	487	2	Q99KA4 mus musculu
8	531	41.7	119	2	Q920E7 mus musculu
9	502	39.5	486	2	Q91207 mus musculu
10	496	39.0	480	2	Q91XEL mus musculu
11	487	38.3	471	2	AAH24289 mus musculu
12	487	38.3	471	2	AAH24289 mus musculu
13	478	37.6	108	2	AAH11048 mus musculu
14	477.5	37.5	606	2	Q6GMZ2 mus musculu
15	475	37.3	464	2	Q6MZU6 mus musculu
16	475	37.3	464	2	CAE45931 mus musculu
17	474.5	37.3	124	2	BAD00233 mus musculu
18	473	37.2	473	2	Q91205 mus musculu
19	471.5	37.1	478	2	Q6P1B1 mus musculu
20	471.5	37.1	478	2	AAH41037 mus musculu
21	470	36.9	106	2	Q9U410 mus musculu
22	470	36.9	124	2	BAD00534 mus musculu
23	469.5	36.9	120	2	BAD00231 mus musculu
24	469.5	36.9	126	2	BAD00225 mus musculu
25	468.5	36.8	125	2	BAD00491 mus musculu
26	468	36.8	122	2	BAD00446 mus musculu
27	467	36.7	98	1	HV57_MOUSE mus musculu
28	467	36.7	119	2	AA135865 lama glam
29	467	36.7	126	2	BAD00420 mus musculu
30	467	36.7	126	2	BAD00529 mus musculu
31	466	36.6	128	2	BAD00406 mus musculu

32	465.5	36.6	470	2	Q6PJA4 homo sapien
33	465.5	36.6	470	2	AAH18747 mus musculu
34	465	36.6	128	2	BAD00444 mus musculu
35	464.5	36.5	119	2	BAD00399 mus musculu
36	464	36.5	122	2	BAD00549 mus musculu
37	464	36.5	126	2	BAD00510 mus musculu
38	463	36.4	117	2	AA135875 lama glam
39	462.5	36.4	136	1	HV16_MOUSE mus musculu
40	462.5	36.4	613	2	Q6WUK1 mus musculu
41	460	36.2	117	1	HV55_MOUSE mus musculu
42	460	36.2	123	1	BAD00234 mus musculu
43	459.5	36.1	97	1	HV56_MOUSE mus musculu
44	459	36.1	437	2	Q9R1A4 mus musculu
45	458.5	36.0	125	2	BAD00448 mus musculu

## ALIGNMENTS

## RESULT 1

ID	Q6KB05	PRELIMINARY;	PRT;	255 AA.
AC	Q6KB05;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Scfv B85 protein (Fragment).			
GN	Name=scfv B85;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRALN=Balb/C;			
RA	Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,			
RA	Briand J.P., Hoebeke J.,			
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AJ746180; CAG34081.1; -			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; Ig; 2.			
DR	SMART; SM00409; Ig; 2.			
DR	SMART; SM00406; Ig; 2.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
FT	NON TER			
FT	1			
SQ	SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;			

Query Match 73.6%; Score 936.5; DB 2; Length 255;  
Best Local Similarity 72.9%; Pred. No. 1.6e-62;  
Matches 180; Conservative 23; Mismatches 33; Indels 11; Gaps 3;

QY	1	QVXKQESGGGLVKGSGSLKSCASGTFPSYKSWRQTPDKRLKLEWVATISGSGSYYY	60
DB	1	QVXKQESGGGLVKGSGSLKSCASGTFPSYKSWRQTPDKRLKLEWVATISGSGSYYY	60
QY	61	PDVYKGRFTISRDAKNTLYLQMSLKSSEDTAMYYCARG--NWEGYFDVWGQTTVTV	117
DB	61	PDVYKGRFTISRDAKNTLYLQMSLKSSEDTAMYYCARG--NWEGYFDVWGQTTVTV	117
QY	118	SSGGGSGGGGSGGGGSGNIELTQSPALMSAPGRVYMTCASSST-----RIYIYQ	170
DB	118	SSGGGSGGGGSGGGGSGNIELTQSPALMSAPGRVYMTCASSST-----RIYIYQ	170
QY	120	SSGGGSGGGGSGGGGSGDIWAQSPSSLSVAGKIVMSCKSSQSLNSRQKYLAVYQ	179
DB	120	SSGGGSGGGGSGGGGSGDIWAQSPSSLSVAGKIVMSCKSSQSLNSRQKYLAVYQ	179
QY	171	QKPSPELLIYDYSNVAVGVPFPFSGSGSTSYSLTINMEADDAATYYCOEMSGVYPT	230
DB	171	QKPSPELLIYDYSNVAVGVPFPFSGSGSTSYSLTINMEADDAATYYCOEMSGVYPT	230
QY	180	QKPSPELLIYDYSNVAVGVPFPFSGSGSTSYSLTINMEADDAATYYCOEMSGVYPT	239
DB	180	QKPSPELLIYDYSNVAVGVPFPFSGSGSTSYSLTINMEADDAATYYCOEMSGVYPT	239
QY	231	FGGGTKL 237	
DB	231	FGGGTKL 237	
QY	240	FGAGTKL 246	
DB	240	FGAGTKL 246	

RESULT 2  
CAG34081 PRELIMINARY; PRT; 255 AA.  
ID CAG34081  
AC CAG34081;  
DT 01-JUN-2004 (Tremblrel. 27, Created)  
DT 01-JUN-2004 (Tremblrel. 27, Last sequence update)  
DT 01-JUN-2004 (Tremblrel. 27, Last annotation update)  
DE scfv B8E5 protein (Fragment).  
GN scfv B8E5.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=balb/c;  
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,  
RA Briand J.P., Hoebeke J.;  
RT "Modulation of the M2 muscarinic receptor activity with monoclonal  
RT anti-M2 receptor antibody fragments."  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ746180; CAG34081.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;  
Query Match 73.6%; Score 936.5; DB 2; Length 255;  
Best Local Similarity 72.9%; Pred. No. 1.6e-62;  
Matches 180; Conservative 23; Mismatches 33; Indels 11; Gaps 3;  
QY 1 QVQLQESGGGLVPRGSGSLKLSKAASGFTPSYGMWVRQTPDKRLKLEWVAITISGGSSTYY 60  
DB 1 QVQLQESGGGLVPRGSGSLKLSKAASGFTPSYGMWVRQTPDKRLKLEWVAITISGGSSTYY 60  
QY 61 PDSYKGFRTISRDNANKNTLYLQMSLKSDEPTAMYYCARG--NMEGYFDVWGQGTIVY 117  
DB 61 PDSYKGFRTISRDNANKNTLYLQMSLKSDEPTAMYYCARHINRYDG-AFDYWGQGTIVY 119  
QY 118 SSGSGGGGGGGSGGSGNIELTQSPALMSASPERVMTCSASSI-----RYIYWQ 170  
DB 120 SSGSGGGGGGGSGGSDIWAQSPSLVSAGSKVMSCKSSQSLNSRNQKNTLYLWYQ 179  
QY 171 QKPGSSPRLIYDTSNVAQVPRFSGSGSGTYSLTINMEADDAATYYCOEWSGYPT 230  
DB 180 QKPGSGSKLIYGSTRESGVPDFTSGSGSTDTLTITSSQADDLAVYYQNHSYPLT 239  
QY 231 FGGSTKL 237  
DB 240 FGAQTKL 246  
ID Q9QYFO PRELIMINARY; PRT; 298 AA.  
AC Q9QYFO;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE CN 8 single chain antibody.  
GN Name=CN 8 scfv;  
OS synthetic construct.  
OC artificial sequences.  
NCBI\_TaxID=32630;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=20183931; PubMed=10706631;  
RA Shinohara N., Demura T., Fukuda H.;  
RT "Isolation of a vascular cell wall-specific monoclonal antibody  
RT recognizing a cell polarity by using a phage display subtraction  
RT method."  
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).  
DR EMBL; AB036341; BAA8653.1; -.  
PIR; A33933; A33933.

DR PIR; S19112; S19112.  
DR HSSP; P01820; 1A70.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PSS0835; IG\_LIKE; 2.  
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;  
Query Match 65.9%; Score 838; DB 2; Length 298;  
Best Local Similarity 68.5%; Pred. No. 4.6e-55;  
Matches 163; Conservative 24; Mismatches 49; Indels 2; Gaps 2;  
QY 1 QVQLQESGGGLVPRGSGSLKLSKAASGFTPSYGMWVRQTPDKRLKLEWVAITISGGSSTYY 60  
DB 40 QVQLQESGGGLVPRGSGSLKLSKAASGSDPRYMSVNRQAPGKLEWGINDSITNY 99  
QY 61 PDSYKGFRTISRDNANKNTLYLQMSLKSDEPTAMYYCARGMEGWYFDVWGQGTIVYSSG 120  
DB 100 TPELTKKFTISRDNANKNTLYLQMSKVRSEDTALYCARAGYQ-HSAVWGQGTIVYSSG 158  
QY 121 GGGSGGGGGGGSGGSGNIELTQSPALMSASPERVMTCSASSI-RYIYWQKPGSSPRL 179  
DB 159 GGGSGGGGGGGSGGSDIELTQSPALMSASVGETVITCRASGNINHTLWYQKPGSSPOL 218  
QY 180 LIYDTSNVAQVPRFSGSGSGTYSLTINMEADDAATYYCOEWSGYPTFGGQTKL 237  
DB 219 LVINAKTLADGVSRFRSGSGSGTQYSLKINSLOPEDPGSYTCQHFMTPTTFPGGQTKL 276

RESULT 4  
Q921A6 PRELIMINARY; PRT; 241 AA.  
ID Q921A6  
AC Q921A6;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Anti-CEA 79 single chain Fv (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=98170165; PubMed=9509426;  
RX Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,  
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;  
RT "Cloning and characterization of cDNAs encoding VH and VL of a  
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and  
RT generation of a single-chain Fv molecule (scfv)."  
RL Mol. Cells 7:816-819(1997).  
DR EMBL; U88067; BAB48044.1; -.  
DR PIR; S19965; S19965.  
DR PIR; S19967; S19967.  
DR PIR; S19968; S19968.  
DR PIR; S26325; S26325.  
DR InterPro; IPR007110; Ig\_1like.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PSS0835; IG\_LIKE; 2.  
FT NON\_TER 1  
SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match 55.9%; Score 710.5; DB 2; Length 241;  
Best Local Similarity 58.3%; Pred. No. 1.4e-45;  
Matches 141; Conservative 34; Mismatches 56; Indels 11; Gaps 5;  
QY 1 QVQLQESGGGLVPRGSGSLKLSKAASGFTPSYGMWVRQTPDKRLKLEWVAITISGGSSTYY 60  
DB 1 QVQLQESGPELKKRGETVKISCKASGYTFDYGMMWVKAQPGKGLKWMGMINITYGEPY 60

```
Qy 61 PDSVKGFTTSDNAKNTLYLQMSLKSEDTAMYYCARGNMGWYFDVWGQTTVTYSSG 120
D 61 AADKRGKFPASLETSASTAYLQINNKLKNEIDTATYFCACKDLR-YFDWGGGTTVTYSSG 119
Qy 121 GGGSGGGSGGGGNIETLQSPAIMSAPGERVTMTCSASSI-RYIYWOQKPGSSPR- 178
D 120 GGGSGGGSGGGGDIETLQSPSSLSALGKVTITCAAGDINKIYAMGHKQKGPSS 179
Qy 179 ---LLIYDTSNVAQVPPRFGSGSGSTYSLTINMEADATYYCOEWSGYPTTGGGT 235
D 180 AHTHAIY---IQGIPERFSGSGSGRYSFISINLEPEDATYCYLHYDWL-HTFGGCT 234
Qy 236 KL 237
D 235 KL 236
```

## RESULT 5

```
Q70M2 PRELIMINARY; PRT; 243 AA.
AC Q70M2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE SCFV 6H8 protein (Fragment).
GN Name=scfv 6H8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=Balb/c;
RX MEDLINE=2285326; PubMed=12860977;
RA Peter J.C., Eftekhari P., Billiard P., Wallukat G., Hoebeke J.;
RT "scfv single chain antibody variable fragment as inverse agonist for
the beta-2 adrenergic receptor."
RL J. Biol. Chem. 278:36740-36747(2003).
DR EMBL; AJ574851; CA000495.1; -.
DR InterPro; IPR007110; IG_1like.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGv_2.
DR PROSITE; PSS0835; IG_LIKE; 2.
FT NON_TER 1
SQ SEQUENCE 243 AA; 25976 MM; BFFPE4D2DCE4FT6 CRC64;
```

```
Query Match 54.4%; Score 692.5; DB 2; Length 243;
Best Local Similarity 56.5%; Pred. No. 3.2e-44;
Matches 135; Conservative 38; Mismatches 59; Indels 7; Gaps 4;
```

```
Qy 1 QVKLQESGGGLVKGSLKSCAASGFTFSSYGMWVRQTPDKLEWVATISSGSGYTY 60
D 1 QVKLQSGSGSELVRGASVTKLSCKASGYTFTYMMHWKQRIHGGLEWIGNIPYSGITNY 60
Qy 61 PDSVKGFTTSDNAKNTLYLQMSLKSEDTAMYYCARGNMGWYFDVWGQTTVTYSSG 120
D 61 DEKFKNGKILTVDTSSSTAYVHLSLASBDAVYVCARG--GRLDVGWAGTTLTVSSG 117
Qy 121 GGGSGGGSGGGGNIETLQSPAIMSAPGERVTMTCSASSI-RYIYWOQKPGSSPR- 179
D 118 GGGSGGGSGGGGDIETLQSPSSLSALGKVTITCAAGDINKIYAMGHKQKGPSS 177
Qy 180 LIYDTSNVAQVPPRFGSGSGSTYSLTINMEADATYYCOE-WSGYPTTGGGTRL 237
D 178 LISGATSLETGVPPRFGSGSGSKDYTLISLTQTEDEVATYYCQQYWS--TRTFGGGTRL 234
```

## RESULT 6

```
Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
```

```
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE MRPS (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after irradiation in mice."
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain."
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
```

```
DR EMBL; AF240168; AAK43733.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 218
SQ SEQUENCE 218 AA; 23013 MM; 527E4FA8F7982817 CRC64;
```

```
Query Match 46.2%; Score 588; DB 2; Length 218;
Best Local Similarity 53.0%; Pred. No. 2e-36;
Matches 115; Conservative 36; Mismatches 60; Indels 6; Gaps 2;
```

```
Qy 1 QVKLQESGGGLVKGSLKSCAASGFTFSSYGMWVRQTPDKLEWVATISSGSGYTY 60
D 3 QVKLQSGSGSELVRGASVTKLSCKASGYTFTYMMHWKQRIHGGLEWIGNIPYSGITNY 62
Qy 61 PDSVKGFTTSDNAKNTLYLQMSLKSEDTAMYYCARGNMGWYFDVWGQTTVTYSSG 120
D 63 ABEFKGKFPASLETSASTAYLQINNKLKNEIDTATYFCCKRWYDGG-FAYWGGGTTVTYSSG 121
Qy 121 GGGSGGGSGGGGNIETLQSPAIMSAPGERVTMTCSASSI---IRYIYWOQKPGS 175
D 122 GGGSGGGSGSGSDIVLTQSPSLAVSLGQRATISCRASEVDNIGISFMMWFOQKPGQ 181
Qy 176 SPRLIYDTSNVAQVPPRFGSGSGSTYSLTINRME 212
D 182 PPKLLIYAASKQSGVPAGLAAGSGTDFSLNIPME 218
```

## RESULT 7

```
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE LOC380791 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
```

RA	Alteichl S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,	
RA	Stegleleim M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Rah S.S., Luquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,	
RA	Boask S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalón D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Falley U., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywinski M.T., Skalska U., Smailus D.E., Scherch A., Schein J.E.,	
RA	Jones S.J., Marra M.A.,	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RM	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-Czech II;	
RC	TISSUE-Mammary tumor metastasized to lung. Tumor arose spontaneously;	
RA	Strausberg R.;	
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBS databases.	
DR	EMBL; BC004786; AAH04786.1; --	
DR	HSSB; F01810; 2FBJ.	
DR	InterPro; IPR007110; Ig-1-like.	
DR	InterPro; IPR003597; Ig_c1.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF07654; C1-set; 2.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS00835; IG_LIKE; 4.	
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 2.	
SQ	SEQUENCE 487 AA; 52554 MW; 7DC98E96DB33077B CRC64;	
Query Match	42.7%; Score 543.5; DB 2; Length 487;	
Beet Local Similarity	50.8%; Pred. No. 1.1e-32;	
Matches 127; Conservative 16; Mismatches 36; Indels 71; Gaps 8;		
QY	1 OYKLESGGGGLVPGGSLKLSCAAGGFPSSYSGMSWVQTPDKRLIEWATTSSGGSYNY 60	
DB	20 EQVLVESGGGLVPGGSLKLSCAAGGFTSSYAMSWVROTPEKRLIEWATTSSDGSYYTY 79	
QY	61 PDVYAGRFTISRDNKNTLYLQMSLSKSDTAMYYCAR---GNMEGWY--PDVWQGGTIV 115	
DB	80 PDNVYAGRFTISRDNKNNLYLQMSHLKSDTAMYYCARMDGSGPYGGISRFYWQGGTTI 139	
QY	116 TVSSGGGGGGGGGGGGGSGGGSNIFLTGSPAI-----MSASFGERYVTMTCSASSIRYTY 167	
DB	140 TVSS-----ESANRPRTYPLTLPRALSDP-----VILIC----- 169	
QY	168 WYQQRPGSSPRLLIYD-----TSNVPF-----VPRFSGSGSGTYSYLTINRM 211	
DB	170 -----LHIDYPPSGTMMNTWKGSKGDIITVNFPPALASGGGYTSSQLTLPRAY 217	
QY	212 EAEDATATYTC 221	
DB	218 ECPGEGSYVC 227	
RESULT 8		
Q920E7	PRELIMINARY; PRT; 119 AA.	
AC	Q920E7:	
DT	01-DEC-2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DE	Pterin-mimicking anti-idiotope heavy chain variable region (Fragment).	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

CC Mammalia Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Atkin J.D., Iape A., Jennings I.G., Horatis O., Cotton R.G.H.;  
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF307937; AL09421.1; -.  
 DR PIR; C25913; C25913.  
 DR HSSP; P01783; 1IGC.  
 DR InterPro; IPR007110; 1G-1like.  
 DR InterPro; IPR003596; 1G\_v.  
 DR Pfam; PF00047; 1g; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; 1G-LIKE; 1.  
 FT NON TER 1  
 FT NON TER 119  
 SQ SEQUENCE 119 AA; 13025 MM; FEB904044381CA7C CRC64;  
 Query Match 41.7%; Score 511; DB 2; Length 119;  
 Best Local Similarity 86.9%; Pred. NO. 2e-32; 7; Indels 6; Gaps 2  
 Matches 106; Conservative 3; Mismatches  
 QY 1 QVKIQESGGGLVKKGGSLKLSCAASGPTFFSSYGMSSWRQTDPDKRLRWATISSGGSYTY 60  
 Db 1 EVOLVESGDLVKKGGSLKLSCAASGPTFFSSYGMSSWRQTDPDKRLRWATISSGGSYTY 60  
 QY 61 PDSYKGRFTTRDRAKNTLYIQMSLKSSEDPTAMTYCARGMEGWY---PDVWGQITVTV 117  
 Db 61 PDSYKGRFTTRDRAKNTLYIQMSLKSSEDPTAMTYCAR---HGDYDVGFAVWGQITLVTV 117  
 QY 118 SS 119  
 Db 118 SA 119  
 RESULT 9  
 Q91Z07 PRELIMINARY; PRT; 486 AA.  
 ID Q91Z07  
 AC 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE LOC380791 protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=Czech II;  
 RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Whitl model.  
 RC Expression driven by an MMTV-LTR enhancer.;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Scheiner C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,  
 Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 Bogak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butcherfield Y.S.,  
 Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,  
 Jones S.J., Mair M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).



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[2]
RN  SEQUENCE FROM N.A.
RP  STRAIN=Czech II;
RC  TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Mut1 model.
RA  Expression driven by an MMTV-LTR enhancer.;
RA  Strausberg R.;
RL  Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC010324; AAH10324.1; -.
DR  HSSP; P01789; IMCP.
DR  InterPro; IPR007110; IG-1like.
DR  InterPro; IPR003597; IG_c1.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF07654; CI-bee; 2.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG LIKE; 4.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ  SEQUENCE 486 AA; 52681 MW; 4FEF835125DA870B CRC64;

Query Match 39.5%; Score 502; DB 2; Length 486;
Best Local Similarity 46.8%; Pred. No. 1,4e-29;
Matches 117; Conservative 21; Mismatches 40; Indels 72; Gaps 8;

OY 1 QVXLOESGGGLVKGSGSLKSCAASGFTFSSYGMWVQTPDKRLKLEWATISSGGSYYTY 60
DB EVHLVESGGGLVKGSGSLKSCVVSFSTSYDSMWVQTEPKRLKLEWATISSGGSYYTY 78
OY 61 PDSVYGRFTISRDNKNTLYIQMSLTKSEDTAMYYCARGN-----WEGMYFDWGGCTTV 115
DB 79 PDNVKGRFTVRDNKNTLYIQMSLTKSEDTAMYYCVRPELPIYYSSSYSDSCGCTTI 138
OY 116 TVSSGGGGGGGGGGGGGSGGSGNIELTQSPAI-----MSASPERVTMTCSASSIRYIY 167
DB 139 TVSS-----ESARNPTIYPLTLPALSSDP-----VILGC----- 168
OY 168 WYQCKPGSSPRLLYD-----TSNVAPG-----VPRFSGSGSGSYSLTINRM 211
DB 169 -----LHIDYPPSGTMMVTWCKSGKIDITTVNFPALASGGGYTWSSQLTLPV 216
OY 212 EAEDATYYC 221
DB 217 ECPGESYKC 226

RESULT 10
O91XE1 PRELIMINARY; PRT; 480 AA.
ID O91XE1;
AC O91XE1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein (Fragment).
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Holys S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnski M.I., Skelton U., Smallie D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010798; AAH10798.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-bee; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 480 AA; 51936 MW; 20B9234EBF2B41BD CRC64;

Query Match 39.0%; Score 496; DB 2; Length 480;
Best Local Similarity 48.1%; Pred. No. 3,9e-28;
Matches 115; Conservative 20; Mismatches 46; Indels 58; Gaps 6;

OY 2 VKLOESGGGLVKGSGSLKSCAASGFTFSSYGMWVQTPDKRLKLEWATISSGGSYYTY 61
DB 20 VKLVESGGGLVKGSGSLKSCAASGFTFSSYGMWVQTEPKRLKLEWATISSGGSYYTY 79
OY 62 DSVYGRFTISRDNKNTLYIQMSLTKSEDTAMYYCARGNMEGYFDWGGCTTVTSSGG 121
DB 80 DSMKGRFTISRDNKNTLYIQMSLTKSEDTAMYYCTGDDY--WYFDWGGCTTVTSS-- 135
OY 122 GSGGGGGGGGGGSGNIELTQSPAIMSASPERVTMTCSASSIRYIYQCKPGSSPRL-- 179
DB 136 -----EPAREPTI-----YPLFPALSSDPYIIG 160
OY 180 -LYD-----TSNVAPG-----VPRFSGSGSGSYSLTINMEADATYYC 221
DB 161 CLHIDYPPSGTMMVTWCKSGKIDITTVNFPALASGGGYTWSSQLTLPVCEPGESYKC 219

RESULT 11
AAH24289 PRELIMINARY; PRT; 471 AA.
ID AAH24289;
AC AAH24289;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

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RA Bosak S., McEwan P.J., McEwan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hade S., Gacie A.W., Gay L.J., Huliy S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Faling J., Hailton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywnicki M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2].  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=5p1een;  
 RA Strauberg R.,  
 RA Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: BC024289; AAH24289.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 471 AA; 51791 MW; 388B7F4CF58660E CRC64;

Query Match	38.3%	Score 487	DB 2	Length 477
Best Local Similarity	46.3%	Pred. No. 1.8e-28		
Matches 105	Conservative 33	Mismatches 61	Indels 28	Gaps 4

```

QY 1 QVTLQSSGGGLVMPGSLKLSGASGFEFTSSGVMWQTPKRLREWATISGGGATYY 60
Db 20 EVQLVDSGGGLVMPGSLRSLGASGFEFTSSGVMWVQAPKGLGLEWSSSSSSYY 79
QY 61 PDSVKGKFTISRDNACTLTLYLQMSLKSSEDITAMYCARGNWE---GWYFDWVGQGVTVV 117
Db 80 ADSVKGRFTISRDNANSLYLQMSLSRADDTAVYCCADLRLQISYWYFDLNGGLTVV 139
QY 118 SSGGGGSGGGGSGGGGNSIELTQSPAIMSGASGFERVTMTCSASSIRIYYQOKPGSSP 177
Db 140 SSAS-----TKGPEVFPLAASSKSTSGGTALCLVKDYFE-----P 177
QY 178 RLILYDTSNVAPEV---PFRSSSGSGCTISLTIRMMEADPATYYC 221
Db 178 VVYSVMNSGALTSGVHTFPFAVLQSSGGLYSLSISVTVVSSSLGTQYIC 224

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RESULT 12			
Q91WPS			
ID	Q91WPS	PRELIMINARY;	PRT; 479 AA.
AC	Q91WPS;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Igh-VJ558 protein.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=FVB/N. TISSUE=Colon;		
RX	MEDLINE=22388257; PubMed=12477932;		
RA	Strasberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemmer C.M., Schuler G.D.,		
RA	Altshul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Dickchenko L., Marsina K., Farmer A.C., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,		
RA	Brownstein W.J., Uddin T.B., Tohyiuki S., Carninci P., Prange C.,		
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McLean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Faney J., Helton E., Ketteman M., Madan A.C., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		

RA Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.:  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";   
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RA Strauberg R.;  
 RL Submitted (SSP-2001) to the EMBL/GenBank/DBJ databases

DR HSSP; P01789; IMCP.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; CI-set; 2.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
SQ SEQUENCE 479 AA; 51603 MW; EC82D0877748584F CEC64;

Query Match	38.3%	Score 487	DB 2	length 479
Best Local Similarly	47.1%	Pred. No. 1.8e-28		
Matches 113	Conservative 19	Mismatches 48	Indels 60	Gaps 6

QY	1	VYKLOESGGGLYKRGSGSLKJLSCASGPFSSYGNMWRQTPDKLEWATLSSGGSYYYY	60
		EVOLVESGGGLYKRGSGSLKJLSCASGGLTFSTNIAHSMWRQSEPKLEWVAALINSNGNTYY	79
Db	20	EVOLVESGGGLYKRGSGSLKJLSCASGGLTFSTNIAHSMWRQSEPKLEWVAALINSNGNTYY	79
QY	61	PDYKRGFTTISRDNAKNTLYLQMSLSKSEPDAMYYCARGNMGWYFDVWGQGTIVYASSG	120
		SDTMKGRFTISRDNAKNTLYLQMSLSKSEPDIAFYCYRCG---YFDVWGAGTAVTASS-	134
Db	80	SDTMKGRFTISRDNAKNTLYLQMSLSKSEPDIAFYCYRCG---YFDVWGAGTAVTASS-	134
QY	121	GGSGGGGGGGGGGNIETGSPAIMSASPGERVTMTCSASSIRITYYQOKPGSSPPL-	179
		-----EPAEPEPTI-----YPLFPALSSDPVIL-	158
Db	135	-----EPAEPEPTI-----YPLFPALSSDPVIL-	158
QY	180	---LTYD---TSNVARG-----VPRFSGSGSGTSYSLTINRMEDADAAATYYC	221
Db	159	GCLLHDFVFPSTGMVWVWKSGLDITTVNFPALASGGGRYTWSSQOLTPAVICPEESVXKC	218

0Y	138	LTGSPAIMSASPGERVTMTCSASSIRIYVYQKPGSSPLLITDTSNVA	PGVPFRFSG	197
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DB 1 MTGPAIMASAPGKVTMTTCASSSVSYMWYQOKPGSSPRLIYDTSNLSAGVYVRFSG 60  
QY 198 SGGSTSYSLTINRMEADDAATYYCQEMSGYPYTFGGGTRKL 237  
DB 61 SGGSTSYSLTISRMEADDAATYYCQOMSSYPWTFGGGTRKL 100

RESULT 14  
Q6GM2 PRELIMINARY; PRT; 606 AA.  
AC Q6GM2;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Primary B-Cells;  
RC MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marulita K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stadleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Uadit T.B., Toshiyuki S., Carlanti P., Prange C.,  
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bozak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalski U., Smallie D.E., Schnerch A., Schein J.E.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN (2)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.L.  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073758; AAH73758.1; -  
DR InterPro; IPR003599; IG\_1.  
DR InterPro; IPR007110; IG\_1-like.  
DR InterPro; IPR003597; IG\_1.  
DR InterPro; IPR003596; IG\_1.  
DR InterPro; IPR003596; IG\_1.  
DR Pfam; PF07654; CI-sect; 4.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGV; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Hypothetical protein.  
SQ SEQUENCE 606 AA; 66184 MW; B6B38B5114E4C55 CRC64;

Query Match 37.5%; Score 477.5; DB 2; Length 606;  
Best Local Similarity 68.3%; Pred. No. 1.2e-27;  
Matches 95; Conservative 12; Mismatches 17; Indels 15; Gaps 2;

QY 1 QVKTQESGGGLVKKPGSLKLSAASGFTFSSYGMWYRQTPDKRLKLEWYATISSGGSYTY 60  
DB 20 QVQLVESGGGLVKKPGSLKLSAASGFTFSSYGMWYRQTPDKRLKLEWYATISSGGSYTY 79  
QY 61 PDVYKGRFTISRDNKNTLYIQWMSLKSEDTAMTYCARGN-----WEGNYF--- 106

DB 80 ADVYKGRFTISRDNKNTLYIQWMSLKSEDTAMTYCARGNGIAGAENVYAEIDYTYTG 139  
QY 107 -DVWGQGTIVTVSSGGGGS 124  
DB 140 MDVWGQGTIVTVSSGGGASA 158

RESULT 15  
Q6MZU6 PRELIMINARY; PRT; 464 AA.  
AC Q6MZU6;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Hypothetical protein DKEP2686C15213.  
OS Name=DKEP2686C15213;  
GN Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Human rectum tumor;  
RC THE GERMAN HUMAN CDNA CONSORTIUM;  
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amlid C., Oeanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640874; CAE45931.1; -  
DR InterPro; IPR003599; IG\_1.  
DR InterPro; IPR007110; IG\_1-like.  
DR InterPro; IPR003597; IG\_1.  
DR InterPro; IPR003596; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; CI-sect; 3.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGV; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match 37.3%; Score 475; DB 2; Length 464;  
Best Local Similarity 59.8%; Pred. No. 1.4e-27;  
Matches 98; Conservative 18; Mismatches 20; Indels 28; Gaps 5;

QY 1 QVKTQESGGGLVKKPGSLKLSAASGFTFSSYGMWYRQTPDKRLKLEWYATISS-GGSYTY 59  
DB 20 EVQLVESGGGLVKKPGSLKLSAASGFTFSSYGMWYRQTPDKRLKLEWYATISSGGSYTY 79  
QY 60 YPDVYKGRFTISRDNKNTLYIQWMSLKSEDTAMTYCARGNWEQNY-FDVWGQGTIVTVSS 118  
DB 80 YADVYKGRFTISRDNKNTLYIQWMSLKSEDTAMTYCARGNWEQNY-FDVWGQGTIVTVSS 137  
QY 119 SGGGGSGGGSGGGGNIETQSPALMSASAPGERVTMTCSASSS 162  
DB 138 SAS-----TKGPSVPLAP-----CSRSTS 157

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